

Result No.	Score	Query Match	Length	DB ID	Description
1	1165	100.0	231	4	US-10-386-972-2 Sequence 2, Appli
2	1160	99.6	231	3	US-08-721-259-2 Sequence 2, Appli
3	1160	99.6	231	4	US-09-611-216-2 Sequence 2, Appli
4	423.5	36.4	265	1	US-07-598-551-2 Sequence 7, Appli
5	422.5	36.4	265	1	US-08-159-610-7 Sequence 7, Appli
6	423.5	36.4	265	1	US-08-129-609A-7 Sequence 7, Appli
7	423.5	36.4	265	1	US-08-435-313-7 Sequence 7, Appli
8	422.5	36.4	265	1	US-08-415-924-2 Sequence 2, Appli
9	423.5	36.4	265	2	US-08-657-579A-2 Sequence 7, Appli
10	423.5	36.4	265	3	US-09-224-025-7 Sequence 7, Appli
11	422.5	36.4	265	4	US-09-706-541-7 Sequence 7, Appli
12	423.5	36.4	265	5	PCT-US94-07887-7 Sequence 7, Appli
13	417	35.8	222	1	US-08-129-610-8 Sequence 8, Appli
14	417	35.8	222	1	US-08-159-603A-8 Sequence 8, Appli
15	417	35.8	222	1	US-08-455-313-8 Sequence 8, Appli
16	417	35.8	222	1	US-08-475-924-3 Sequence 3, Appli
17	417	35.8	222	2	US-08-657-579A-3 Sequence 3, Appli
18	417	35.8	222	3	US-09-224-025-8 Sequence 8, Appli
19	417	35.8	222	4	US-09-706-541-8 Sequence 8, Appli
20	417	35.8	222	5	PCT-US94-07887-8 Sequence 4, Appli
21	97	8.3	1833	4	US-08-621-943A-4 Sequence 4, Appli
22	97	8.3	1833	4	US-08-945-575D-4 Sequence 3, Appli
23	97	8.3	1992	4	US-08-621-943A-3 Sequence 3, Appli
24	97	8.3	1992	4	US-08-945-575D-3 Sequence 3, Appli
25	97	8.3	2048	3	US-09-268-347-48 Sequence 48, Appli
26	93	8.0	2123	3	US-08-948-683A-10 Sequence 10, Appli
27	89.5	7.7	624	4	US-09-248-796A-24363 Sequence 24363, A

Patent No. 6093695
 GENERAL INFORMATION:
 APPLICANT: Rupar, Mark J.
 APPLICANT: Donovan, William P.
 APPLICANT: Tan, Yiping
 APPLICANT: Slaney, Annette C.
 TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET29
 TITLE OF INVENTION: COMPOSITIONS TOXIC TO COLEOPTERAN
 TITLE OF INVENTION: INSECTS AND CTENOCEPHALIDES spp.
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION NUMBER: US/09/611,216
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: MOBT:017
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 231 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE CHARACTERISTICS:
 LENGTH: 231 amino acids
 TOPology: linear
 MOLECULE TYPE: protein
 US-09-611-259-2

Query Match 99.6%; Score 1160; DB 3; Length 231;
 Best Local Similarity 99.6%; Pred. No. 8.6e-111;
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFENRVTITLTVSSDVNVYSEIYQVAPQYINQALTLAKYFQGAIDGSTLRFDEKALQIA 60
 Db 1 MFENRVTITLTVSSDVNVYSEIYQVAPQYINQALTLAKYFQGAIDGSTLRFDEKALQIA 60
 Qy 61 NDIPQAQAVNTLNQTVQGTQVSYNIDKIVDIMKQVLSTVDNCKFWDQVTAATNTFT 120
 Db 61 NDIPQAQAVNTLNQTVQGTQVSYNIDKIVDIMKQVLSTVDNCKFWDQVTAATNTFT 120
 Qy 121 NLNSQESAEWIFFYKEDAHKTSYYNNILFAQDEETGGMAMTLPADISVDIEKEKVLF 180
 Db 121 NLNSQESAEWIFFYKEDAHKTSYYNNILFAQDEETGGMAMTLPADISVDIEKEKVLF 180
 Qy 181 VTIKDTEINYATVKAINVVOALQSRSDKVDAFSPRHLPRKRKICNS 231
 Db 181 VTIKDTEINYATVKAINVVOALQSRSDKVDAFSPRHLPRKRKICNS 231

RESULT 4
 US-07-958-551-2
 Sequence 2, Application US/09611216
 Patent No. 6537756
 GENERAL INFORMATION:
 APPLICANT: Rupar, Mark J.
 APPLICANT: Donovan, William P.
 APPLICANT: Tan, Yiping
 APPLICANT: Slaney, Annette C.
 TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET29
 TITLE OF INVENTION: COMPOSITIONS TOXIC TO COLEOPTERAN

TITLE OF INVENTION: INSECTS AND CTENOCEPHALIDES spp.
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/611,216
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/611,216
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE/DOCKET NUMBER: MOBT:017
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 231 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-611-216-2

Query Match 99.6%; Score 1160; DB 4; Length 231;
 Best Local Similarity 99.6%; Pred. No. 8.6e-111;
 Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFENRVTITLTVSSDVNVYSEIYQVAPQYINQALTLAKYFQGAIDGSTLRFDEKALQIA 60
 Db 1 MFENRVTITLTVSSDVNVYSEIYQVAPQYINQALTLAKYFQGAIDGSTLRFDEKALQIA 60
 Qy 61 NDIPQAQAVNTLNQTVQGTQVSYNIDKIVDIMKQVLSTVDNCKFWDQVTAATNTFT 120
 Db 61 NDIPQAQAVNTLNQTVQGTQVSYNIDKIVDIMKQVLSTVDNCKFWDQVTAATNTFT 120
 Qy 121 NLNSQESAEWIFFYKEDAHKTSYYNNILFAQDEETGGMAMTLPADISVDIEKEKVLF 180
 Db 121 NLNSQESAEWIFFYKEDAHKTSYYNNILFAQDEETGGMAMTLPADISVDIEKEKVLF 180
 Qy 181 VTIKDTEINYATVKAINVVOALQSRSDDKVDAFSPRHLPRKRKICNS 231
 Db 181 VTIKDTEINYATVKAINVVOALQSRSDDKVDAFSPRHLPRKRKICNS 231

RESULT 3
 US-09-611-216-2
 Sequence 2, Application US/09611216
 Patent No. 6537756
 GENERAL INFORMATION:
 APPLICANT: Rupar, Mark J.
 APPLICANT: Donovan, William P.
 APPLICANT: Tan, Yiping
 APPLICANT: Slaney, Annette C.
 TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET29
 TITLE OF INVENTION: COMPOSITIONS TOXIC TO COLEOPTERAN

CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/958,551
 FILING DATE: October 19, 1992
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/788,654
 FILING DATE: No. 5302387ember 6, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: M/J 101.C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 STRAIN: neoleoensis
 INDIVIDUAL ISOLATE: PS201T6
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
 CLONE: 201T635
 US-07-958-551-2

Query Match Score 423.5; DB 1; Length 265;
 Best Local Similarity 40.9%; Pred. No. 3e-35;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVIITLTPSSDVNVSEIYQVA---PQYINQALTLAKYFGQAI----DGSTLRDFE 54
 Db 38 RVIYLKV--KDPDTTQLETTBIEENPVQLQIAQIAFDALVPTETGEAIRFSMP 95
 Qy 55 KALQIANDI-PQAIVVNTLNQTVQQGTVQSYMDIKVDDIMKNVLNSIVDNKKFWDQVTA 113
 Db 96 KGLEVATIQPGAVVAYTDQTLQSNNQVSNNQVSMDRVISVLTQVGMVALSG-SITQDITA 154
 Qy 114 AITNTFTNLNSQEANTFYYKEDAHKTYKAINVYQALQSSRDSKVD---AFKSPRHL 220
 Db 155 ATIDTFNLTQDSANFWGETSHOTNTVNMPAQNETGGRMMCPIGFBFRVFT 214
 Qy 174 EKEKVLFTVIKDTENYAVTKAINVYQALQSSRDSKVD---AFKSPRHL 220
 Db 215 DRRTVLFLTTKDYANTSVNQICLRFAGPLDSRLSINDLSEALRSSKYL 264

RESULT 5
 US-08-129-610-7
 Sequence 7, Application US/08129610
 Patent No. 5436002
 GENERAL INFORMATION:
 APPLICANT: Jewel Payne
 APPLICANT: Kenneth Narva
 APPLICANT: Kendrick Akira Uyeda
 APPLICANT: Christine Julie Stalder
 APPLICANT: Tracy Ellis Michaels

TITLE OF INVENTION: No. 5436002el *Bacillus thuringiensis* Isolates and Toxins
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0., Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/129,610
 FILING DATE:
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/093,199
 FILING DATE: 15-JUL-1993
 NAME:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,350
 FILING DATE: 17-NOV-1992
 NAME:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/746,751
 FILING DATE: 21-AUG-1991
 NAME:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,266
 FILING DATE: 28-MAY-1991
 NAME:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/647,399
 FILING DATE: 29-JAN-1991
 NAME:
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MA55CCD.C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEXFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 STRAIN: neoleoensis
 INDIVIDUAL ISOLATE: PS201T6
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
 CLONE: 201T635
 US-08-129-610-7

Query Match Score 423.5; DB 1; Length 265;
 Best Local Similarity 40.9%; Pred. No. 3e-35;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;
 Qy 5 RVIITLTPSSDVNVSEIYQVA---PQYINQALTLAKYFGQAI----DGSTLRDFE 54
 Db 38 RVIYLKV--KDPDTTQLETTBIEENPVQLQIAQIAFDALVPTETGEAIRFSMP 95
 Qy 55 KALQIANDI-PQAIVVNTLNQTVQQGTVQSYMDIKVDDIMKNVLNSIVDNKKFWDQVTA 113
 Db 96 KGLEVATIQPGAVVAYTDQTLQSNNQVSNNQVSMDRVISVLTQVGMVALSG-SITQDITA 154
 Qy 114 AITNTFTNLNSQEANTFYYKEDAHKTYKAINVYQALQSSRDSKVD---AFKSPRHL 220
 Db 155 ATIDTFNLTQDSANFWGETSHOTNTVNMPAQNETGGRMMCPIGFBFRVFT 214
 Qy 174 EKEKVLFTVIKDTENYAVTKAINVYQALQSSRDSKVD---AFKSPRHL 220
 Db 215 DRRTVLFLTTKDYANTSVNQICLRFAGPLDSRLSINDLSEALRSSKYL 264

RESULT 5
 US-08-129-610-7
 Sequence 7, Application US/08129610
 Patent No. 5436002
 GENERAL INFORMATION:
 APPLICANT: Jewel Payne
 APPLICANT: Kenneth Narva
 APPLICANT: Kendrick Akira Uyeda
 APPLICANT: Christine Julie Stalder
 APPLICANT: Tracy Ellis Michaels

Db 96 KLEVAKTIQPKGAVVAYDTQTSQSNQNQVSYMDRVISVULKTVNGVALSG-SITOLTA 154
 Qy 114 AITNTFTNLSQSEAWIPIYYKEDANKTSTYYNNLFAIQDEBETGGUMATPLIAFDISVDI 173
 Db 155 AITDTFTNLNTQDSDAWFWGKESTSQTNTYNNMPAIONETTGRVMMCYPIGEFLRVFT 214
 Qy 174 EKEKVLFPTIDKTENTAVTKAINVVAQLQSSRSKVD--AFPSPRHL 220
 Db 215 DKRTVLFPTTDYANXNQTLRFQPLIDSRLSINDLSERASSKVL 264

RESULT 6
 US-08-129-609A-7
 Sequence 7, Application US/08129609A
 GENERAL INFORMATION:
 APPLICANT: Jewel Payne
 APPLICANT: M. Keith Kennedy
 APPLICANT: H. Ernest Schnepp
 APPLICANT: David Orlin Brower
 APPLICANT: John Brooks Randal
 TITLE OF INVENTION: Bacillus thuringiensis Isolates Active Toxins
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/129,609A
 FILING DATE: 30-SEP-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/958,551
 FILING DATE: 19-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/788,654
 FILING DATE: 6-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 ORIGINAL SOURCE:
 ORGANISM: Bacillus thuringiensis
 STRAIN: neoleonis
 INDIVIDUAL ISOLATE: PS2016
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGem (TM) -11 Library of Kenneth E. Narva
 CLONE: 201T35

Query Match Similarity 36.4%; Score 423.5; DB 1; Length 265;
 Best Local Similarity 40.9%; Pred. No. 3e-35;

Matches 94; Conservative 47; Mis-matches 72; Indels 17; Gaps 6;
 Qy 5 RVIITTPSSDVNVYSEIYQV---POXINGALILAKYFOGAI----DGSTLPRDFE 54
 Db 38 RVITYKV--KDPIDTQOLLEITEINPNPYLQAOIALAAAFQDALVPTETEFGEARFSMP 95
 Qy 55 KALQZANDI-PQAAVNTLNQTVQDGTQVSYMIKVIDMKNVTSIVIDNKKFNDQVTA 113
 Db 96 KGLEVAKTIQPKGAVVAYDTQTLSSRNQYSWMIIRVISVULKTVNGVALSG-SITOLTA 154
 Qy 114 AITNTFTNLSQESAWIIFYKEDAHKTSTYYNLLFAIQDEBETGGUMATPLIAFDISVDI 173
 Db 155 AITDTFTNLNTQDSDAWFWGKESTSQTNTYNNMPAIONETTGRVMMCYPIGEFLRVFT 214
 Qy 174 EKEKVLFPTIDKTENTAVTKAINVVAQLQSSRSKVD--AFPSPRHL 220
 Db 215 DKRTVLFPTTDYANXNQTLRFQPLIDSRLSINDLSERASSKVL 264

RESULT 7
 US-08-455-313-7
 Sequence 7, Application US/08455313
 PATENT NO. 5635480
 GENERAL INFORMATION:
 APPLICANT: Jewel Payne
 APPLICANT: Kenneth Narva
 APPLICANT: Kendrick Akira Iyeda
 APPLICANT: Christine Julie Stalder
 APPLICANT: Tracy Ellis Michaels
 TITLE OF INVENTION: No. 5635480e1 Bacillus thuringiensis Isolates and Toxins
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/455,313
 FILING DATE: 31-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/129,610
 FILING DATE: 30-SEP-1993
 APPLICATION NUMBER: US/08/093,199
 FILING DATE: 15-JUL-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/093,199
 FILING DATE: 17-NOV-1992
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,266
 FILING DATE: 28-MAY-1991
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/647,399
 FILING DATE: 29-JAN-1991
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGem (TM) -11 Library of Kenneth E. Narva
 CLONE: 201T35

Query Match Similarity 36.4%; Score 423.5; DB 1; Length 265;
 Best Local Similarity 40.9%; Pred. No. 3e-35;

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 STRAIN: *neoleoensis*
 INDIVIDUAL ISOLATE: PS201T6
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
 CLONE: 201T635

US-08-455-313-7

Query Match Score 423.5%; DB 1; Length 265;
 Best Local Similarity 40.9%; Pred. No. 3e-35; Gaps 6;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVIITLPPSSDVNYSRIVQYVA---POYNNQALTLAKYFGQAI----DGSTLRFDFE 54
 Db 38 RVIYLKV--KDPIDTQOLLETEIENPNVYLOQIAQLAAAFQDALVPTETEGERAISMP 95

Qy 55 KALQIANDI-PQAAYVNTLNQTVQGQTQVQSYWIKDVKIDMKNVLSIVIDNKFWQDTA 113
 Db 96 KGLEVAKTIQPGAVVAYTDQTLSQSNQVSYWIMDRVSVLKTVMSVLSG-SIIQLTIA 154

Qy 114 AITNTFPNLNSQEAWMIFYKKEDAKTSYYNNLRAIQDEETGGUMATLPIAFDISYDI 173
 Db 155 AITDTPFLNLNTQOKDSAWFWKGTSIQTNTVNYNMVPAIQNETTGRVMCVPIGFEIRVFT 214

Qy 174 BKEKVLFPVTIKDTENTAVTKAINVVOAQLQSSRSKVD---AFKSPRHL 220
 Db 215 DKRTVLFITKDYANVSNIQTLRFAQPLIDSRLSINDLSEALRSSKYL 264

RESULT 8
 US-08-475-924-2
 Sequence 2, Application US/08475924
 Patent No. 5723440
 GENERAL INFORMATION:
 APPLICANT: Stockhoff, Brian
 ATTORNEY: Conlan, Christopher
 TITLE OF INVENTION: CONTROLLING HEMIPTERAN INSECT PESTS
 TITLE OF INVENTION: WITH *BACILLUS THURINGIENSIS*
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/657,579A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MA96
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 STRAIN: *neoleoensis*
 INDIVIDUAL ISOLATE: PS201T6
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGem (TM)-11 Library of Kenneth E. Narva
 CLONE: 201T635

US-08-475-924-2

Query Match Score 423.5%; DB 1; Length 265;
 Best Local Similarity 40.9%; Pred. No. 3e-35; Gaps 6;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVIITLPPSSDVNYSRIVQYVA---POYNNQALTLAKYFGQAI----DGSTLRFDFB 54
 Db 38 RVIYLKV--KDPIDTQOLLETEIENPNVYLOQIAQLAAAFQDALVPTETEGERAISMP 95

Qy 55 KALQIANDI-PQAAYVNTLNQTVQGQTQVQSYWIKDVKIDMKNVLSIVIDNKFWQDTA 113
 Db 96 KGLEVAKTIQPGAVVAYTDQTLSQSNQVSYWIMDRVSVLKTVMSVLSG-SIIQLTIA 154

Qy 114 AITNTFPNLNSQEAWMIFYKKEDAKTSYYNNLRAIQDEETGGUMATLPIAFDISYDI 173
 Db 155 AITDTPFLNLNTQOKDSAWFWKGTSIQTNTVNYNMVPAIQNETTGRVMCVPIGFEIRVFT 214

Qy 174 BKEKVLFPVTIKDTENTAVTKAINVVOAQLQSSRSKVD---AFKSPRHL 220
 Db 215 DKRTVLFITKDYANVSNIQTLRFAQPLIDSRLSINDLSEALRSSKYL 264

RESULT 9
 US-08-657-579A-2
 Sequence 2, Application US/08657579A
 Patent No. 5885963
 GENERAL INFORMATION:
 APPLICANT: Stockhoff, Brian
 ATTORNEY: Conlan, Christopher
 TITLE OF INVENTION: CONTROLLING HEMIPTERAN INSECT PESTS
 TITLE OF INVENTION: WITH *BACILLUS THURINGIENSIS*
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Saliwanchik & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/657,579A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MA96
 TELECOMMUNICATION INFORMATION:

REGISTRATION NUMBER: 39,355
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 352-315-8100
 TELEFAX: 352-372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 SPAIN: neoleonensis
 INDIVIDUAL ISOLATE: PS201T6
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGem (TM) -11 Library of Kenneth E. Narva
 CLONE: 2011635
 US-08-657-579A-2

Query Match 36.4%; Score 423.5; DB 2; Length 265;
 Best Local Similarity 40.9%; Pred. No. 3e-35; Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVIITLTVPSDVNVYSEIYQVA---PQQYNQALTAIAYKFGGAI----DGSTURDFDE 54
 .Db 38 RVIYLVY--KDPIDTQLEITEIENPVYQIAQAAQDALVPTETEFGEARFSMP 95

Qy 55 KALQIANDI-I-PQAAVNTLNQSEAWMPEAKDHTSKYYNNILPAIDDEETGGYMTAPIADPSVDI 113
 Db 96 KGLEVAKTIQPGAVVAYTDQLSQNNQSVMDRIVSLLTKTNGVALSG-STITQLTA 154

Qy 114 AITNTTPNLNSQEEAWMPEAKDHTSKYYNNILPAIDDEETGGYMTAPIADPSVDI 173
 Db 155 AITDTEPNLNTQDKSAWFWKGSETSHQTNTYNNMFAIONNETTGRRVMMCPIGGFPRVFT 214

Qy 174 EKEKVLFVTTKDENTAVTVAINVQALQSSRSKVD--AFKSPrHL 220
 Db 215 DKRTVLFITTDYANYSVNQIQTLRFAQPLIDSRLSINDLSBEALKSSKYL 264

RESULT 10
 US-09-224-025-7
 Sequence 7 Application US/09224025
 Patent No. 6150165
 GENERAL INFORMATION:
 APPLICANT: Jewel Payne
 APPLICANT: Kenneth Narva
 APPLICANT: Kendrick Akira Ueda
 APPLICANT: Christine Julie Stalder
 APPLICANT: Tracy Ellis Michael
 TITLE OF INVENTION: No. 6150165e1 *Bacillus thuringiensis* Isolates and Toxins
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: David R. Salivanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/224, 025
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/455,313
 FILING DATE: 08/09/93,199
 APPLICATION NUMBER: US 08/093,199
 FILING DATE: 15-JUL-1993
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,350
 FILING DATE: 17-NOV-1992
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/746,751
 FILING DATE: 21-AUG-1991
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,266
 FILING DATE: 28-MAY-1991
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/647,399
 FILING DATE: 29-JAN-1991
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Salivanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MASSCCD.C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-371-5800
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 STRAIN: neoleonensis
 INDIVIDUAL ISOLATE: PS201T6
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGem (TM) -11 Library of Kenneth E. Narva
 CLONE: 2011635
 US-09-224-025-7

Query Match 36.4%; Score 423.5; DB 3; Length 265;
 Best Local Similarity 40.9%; Pred. No. 3e-35; Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVIITLTVPSDVNVYSEIYQVA---PQINQALTAKYFGGAI----DGSTURDFDE 54
 .Db 38 RVIYLVY--KDPIDTQLEITEIENPVYQIAQAAQDALVPTETEFGEARFSMP 95

Qy 55 KALQIANDI-I-PQAAVNTLNQSEAWMPEAKDHTSKYYNNILPAIDDEETGGYMTAPIADPSVDI 113
 Db 96 KGLEVAKTIQPGAVVAYTDQLSQNNQSVMDRIVSLLTKTNGVALSG-STITQLTA 154

Qy 114 AITNTTPNLNSQEEAWMPEAKDHTSKYYNNILPAIDDEETGGYMTAPIADPSVDI 173
 Db 155 AITDTEPNLNTQDKSAWFWKGSETSHQTNTYNNMFAIONNETTGRRVMMCPIGGFPRVFT 214

Qy 174 EKEKVLFVTTKDENTAVTVAINVQALQSSRSKVD--AFKSPrHL 220
 Db 215 DKRTVLFITTDYANYSVNQIQTLRFAQPLIDSRLSINDLSBEALKSSKYL 264

RESULT 11
 US-09-706-541-7
 Sequence 7 Application US/09224025
 Patent No. 6689743
 GENERAL INFORMATION:
 APPLICANT: Jewel Payne

SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 SPAIN: neoleonensis
 INDIVIDUAL ISOLATE: PS201T6
 IMMEDIATE SOURCE:
 LIBRARY: LambdaGem (TM) -11 Library of Kenneth E. Narva
 CLONE: 2011B35
 PCT-US94-07887-7

Query Match 36.4%; Score 423.5; DB 5; Length 265;
 Best Local Similarity 40.9%; Pred. No. 3e-35; Gaps 6;
 Matches 94; Conservative 47; Mismatches 72; Indels 17;

Qy 5 R VITLTVPSDVNTSBIQVAA----POYNNQALTAIAYKFGAI-----DGSTDURFDFE 54
 Db 38 RVIYLKV--KDPIDTQLEITEIENPVYVQAIQAAAFDALVPTETEGEARFSPMP 95

Qy 55 KALQIANDI-I-POAAYVNTLNQVQGTVQYVSMIDKIVDIMKVNLSIVDQNKKFWDQVTA 113
 Db 96 KGLEVAKTIQPKGAVVAYTDTQSNSNQVSVMIDVISVLTQVNGVAISG-SITQLTA 154

Qy 114 AITNTFNLINQSESEAIFIYKEDAHKTYYNNILPAIDDEETGGYMATPLIAFDISVDI 173
 Db 155 AITDTETNLNTQKDSAWFWNGKETSHQTNTYNNMFAIONNETGRMMCPIGPEIRVPT 214

Qy 174 EKBKVLFVFTIKDTDENTAVTVKAIVVQALQGSRSKVD---AFKSPRHL 220
 Db 215 DKRTVLFITTDYANTSVNIQTLRFAQPLIDSRLSINDLSEALRSSKYL 264

RESULT 13 US-08-129-610-8
 Sequence 8, Application US/08129610
 Patent No. 5436002

GENERAL INFORMATION:
 APPLICANT: Jewel Payne
 APPLICANT: Kenneth Narva
 APPLICANT: Kendrick Akira Ueda
 APPLICANT: Christine Julie Stalder
 APPLICANT: Tracy Ellis Michaelis
 TITLE OF INVENTION: No. 5436002el *Bacillus thuringiensis* Isolates and Toxins
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSES: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/129,610
 FILING DATE: 15-JUL-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/093,199
 FILING DATE: 17-NOV-1992

NAME: PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/746,751
 FILING DATE: 21-AUG-1991
 NAME: PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,266
 FILING DATE: 28-MAY-1991
 NAME: PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/647,399
 FILING DATE: 29-JAN-1991
 NAME: ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: MASSCCD.C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEXFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 222 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 STRAIN: neleoenensis
 INDIVIDUAL ISOLATE: PS201T6
 US-08-129-610-8

Query Match 35.8%; Score 417; DB 1; Length 222;
 Best Local Similarity 41.9%; Pred. No. 1.e-34;
 Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

Qy 15 DVNVNSEIYQVA-PQYNNQALTAKYFOGAI----DGSTLRFPEKALQIANDI-PQA 66
 Db 6 DTTQQLIEITEENPVYVQIQLAAAFQDVALVPTETEGEARFSPMPKGLEVAKTIQPKG 65

Qy 67 AVNTLNUQVGTQYQSYWVNDKIVDKNQVNLIVDNRKFWDQVTAATNTPTNINSQ 126
 Db 66 AVVATDQTLQSNNQVSVMIDRVISVLRTVYMGVALSG-SIUTQLTAAITDTFTNINTQ 124

Qy 127 SEAIFIYKEDAHKTSYYNNILFAIDDEETGGYMATPLIAFDISVDIKEKVLFYTTIKDT 186
 Db 125 DSAWFWKGETSKHOTNTYNNMFAIQNETGRMMCPIGPEIRVFTDKRTVFLFLTKDY 184

Qy 187 ENVATVKAIVVQALQGSRSKVD---AFKSPRHL 220
 Db 185 ANYSNQIQTLRFAQPLIDSRLSINDLSEALRSSKYL 221

RESULT 14 US-08-129-609A-8
 Sequence 8, Application US/08129609A
 Patient No. 5489432
 GENERAL INFORMATION:
 APPLICANT: Jewel Payne
 APPLICANT: M. Keith Kennedy
 APPLICANT: John Brookes Randall
 APPLICANT: David Orlin Brower
 APPLICANT: H. Ernest Schneef
 TITLE OF INVENTION: *Bacillus thuringiensis* Isolates Active Against Cockroaches and Genes Encoding Cockroach-Active Toxins
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSES: David R. Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville

STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/129,609A
 FILING DATE: 30-SEP-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/958,551
 FILING DATE: 19-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/788,654
 FILING DATE: 6-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: M/J 101.02
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 222 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Bacillus thuringiensis*
 STRAIN: neoleensis
 INDIVIDUAL ISOLATE: PS201T6
 .US-08-129-609A-8

Query Match Score 417; DB 1; Length 222;
 Best Local Similarity 41.9%; Pred. No. 1.1e-34;
 Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

Qy 15 DVVNYSSEIYQVA-PQYNNQALTLAKYFGQAI-----DGSTIRPDEBKALQIANDI-PQA 66
 Db 6 DTTQLSLTEITENPVYQIAQIAAAQFDALVPTETEGAIRFSMPKGLEVAKTIQPKG 65

Qy 67 AVNTLNQTVQGTQVSMDKIDVIMKAVLIVDNKWDQTAAITNTFTNNSQ 126
 Db 66 AAVAYDTQLSQQNNQVSMIDRVISVTKTNGVALSG-SITQDPAATIDFTNNTQK 124

Qy 127 SEAWIFTYKEDAHKTSTYYNILFAIQDGETGGVMMATPLIAFDISVDEKEKVLFYTQKD 186
 Db 125 DSAWVPMKGKTSQNTNTYNNMFAIQNETTERGVMMCVPGEPIRVTFLTFLTQD 184

Qy 187 ENYAVTYKAINTVQALOSRSRDKVVD--AFKSPRL 220
 Db 185 ANYSVNTQTLRPAQPLIDSRAISINDSEARSSKVL 221

RESULT 15 35.8%; Score 417; DB 1; Length 222;
 Best Local Similarity 41.9%; Pred. No. 1.1e-34;
 Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;

Qy 15 DVVNYSSEIYQVA-PQYNNQALTLAKYFGQAI-----DGSTIRPDEBKALQIANDI-PQA 66
 Db 6 DTTQLSLTEITENPVYQIAQIAAAQFDALVPTETEGAIRFSMPKGLEVAKTIQPKG 65

Qy 67 AVNTLNQTVQGTQVSMDKIDVIMKAVLIVDNKWDQTAAITNTFTNNSQ 126
 Db 66 AAVAYDTQLSQQNNQVSMIDRVISVTKTNGVALSG-SITQDPAATIDFTNNTQK 124

Qy 127 SEAWIFTYKEDAHKTSTYYNILFAIQDGETGGVMMATPLIAFDISVDEKEKVLFYTQKD 186
 Db 125 DSAWVPMKGKTSQNTNTYNNMFAIQNETTERGVMMCVPGEPIRVTFLTFLTQD 184

Qy 187 ENYAVTYKAINTVQALOSRSRDKVVD--AFKSPRL 220
 Db 185 ANYSVNTQTLRPAQPLIDSRAISINDSEARSSKVL 221

Sequence 8, Application US/08455313
 Sequence No. 5635480
 GENERAL INFORMATION:
 APPLICANT: Jewel Payne
 APPLICANT: Kenneth Narva
 APPLICANT: Kendrick Akira Ueda
 APPLICANT: Christine Julie Stalder
 APPLICANT: Tracy Ellis Michaelis
 TITLE OF INVENTION: No. 5635480el *Bacillus thuringiensis* Isolates and Toxins
 NUMBER OF SEQUENCES: 10

Db 125 DSAWVPGKERTSHQTYTYNNMFAIQNETTERGVMMCVPIGEIRVFTDKRTYFLTTKDY 184
Qy 187 ENYAVTVKAINVVAQALOSRDSKVVD--AFKSPRHL 220
Db 185 ANYSVNIQTLRFAQPLIDSRALSINDLSEALRSSKYL 221

Search completed: June 26, 2005, 16:07:05
Job time : 45 secs

Gencore version 5.1.6	P59448	buchnera ap					
Copyright (c) 1993 - 2005 Compugen Ltd.	Q9K9Y9	bacillus ha					
1 Protein - protein search, using SW model	Q9A062	bacharomyces					
on: June 26, 2005, 15:47:47 ; Search time 174 Seconds 679.829 Million cell updates/sec	Q7QH6	giardia lam					
title: US-10-767-605-2	Q8Ieh1	bacillus ce					
perfect score: 1165	Q8Kenz	picrophilus					
Sequence: 1 MFFHRVITLTVPSSDVNNYS.....DAFFSPRHLPRKRHKICNSNS 231	Q8RTH6	fusobacteri					
Scoring table: BL003N62	Q9P008	ureaplasma					
Gapopen: 10.0 , Gapext 0.5	Q7RSG0	plasmid					
Searched: 1612378 seqs, 5120791.87 residues	Q7nbj7	mycoplasma					
Total number of hits satisfying chosen parameters:	1612378	Q8x1x7	clostridium				
minimum DB seq length: 0	Q8Tcm2	plasmid					
maximum DB seq length: 2000000000	Q6Lbz7	plasmid					
st-processing: Minimum Match 0%	Q8Iezz	plasmid					
Maximum Match 100%	Q8Ies4	plasmid					
Listing First 45 summaries	Q8TB54	plasmid					
database : UniProt_03;*		ALIGNMENTS					
1: uniprot_sprot:*							
2: uniprot_trembl:*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
built No.	Score	Query	Match	Length	DB ID	Description	
1	1160	99.6	231	2	Q93M48	Q93m48	PRELIMINARY;
2	637	54.7	259	1	CYAA_BACTY	Q93M48;	PRT; 231 AA.
3	637	54.7	259	2	Q71Kw8	Q93M48;	AC
4	597	51.2	260	2	QBYNKO	Q93M48;	DT
5	595	51.1	263	1	CYBA_BACTY	Q93M48;	DT
6	592.5	50.9	263	1	CYBB_BACTY	Q93M48;	DT
7	586	50.3	263	1	Q9J878	Q93m48	DT
8	456	39.1	249	1	CXAA_BACTY	Q93M48;	DT
9	448	38.5	157	2	Q5298	Q93M48;	DT
10	448	38.5	157	2	Q7BVd4	Q93M48;	DT
11	444	38.1	156	2	O30895	Q93M48;	DT
12	443	38.0	156	2	Q9R9C0	Q93m48	DT
13	442	37.9	156	2	O30969	Q93m48	DT
14	423.5	36.4	265	1	CXBA_BACTY	Q93M48;	DT
15	416.5	35.8	250	1	CKAB_BACTY	Q93M48;	DT
16	344.5	29.6	525	2	Q8KRQ9	Q93M48;	DT
17	151.5	13.0	217	2	Q6USC4	volvariella	DT
18	105.5	9.1	880	2	Q9J9RS	clostridium	DT
19	105.5	9.1	1830	2	Q7YYVO	cryptosporidium	DT
20	105.5	9.1	2528	2	Q863J6	dictyosteli	DT
21	103	8.8	477	2	Q94594	helicobacete	DT
22	103	8.8	477	2	Q25326	helicobacete	DT
23	102.5	8.8	981	2	Q6NET8	parachlamyd	DT
24	101	8.7	477	2	Q9ZLm7	helicobacete	DT
25	99.5	8.5	4540	1	DYHC_PARTB	paramecium	DT
26	98.5	8.5	201	1	Y007_NPYAC	autographa	DT
27	97.5	8.4	1442	2	Q8i858	nilgavarrava	DT
28	96.5	8.3	566	2	Q6CT48	kluyveromyces	DT
29	96.5	8.3	343	1	HRCA_BACSU	p25499 bacillus su	DT
30	95.5	8.2	421	1	TYH_MYCCE	ordm5 mycoplasma	DT
31	95.5	8.2	1876	1	OBON5	at rantoococci	DT
					ID CYA_BACTY	004470;	RESULT 2
					STANDARD;	AC	
					PRT;	259 AA.	

DT	15-JUL-1998 (Rel. 36, Created)	FT	TURN	238	Score 637; DB 1; Length 259;
DT	25-OCT-2004 (Rel. 45, Last annotation update)	SQ	SEQUENCE	259 AA:	29235 NW; 6924A01103D32B51 CRC64;
DE	Type-2Aa cytolytic delta-endotoxin (29 kDa cytolytic toxin).	Query Match	54.7%; Best Local Similarity 56.0%; Pred. No. 2, 9e-40;		
GN	Name=cyr2Aa1; Synonyms=cytB;	Matches	126; Conservative 43; Mismatches 54; Indels 2; Gaps 2;		
OS	Bacillus thuringiensis (subsp. <i>kyushuensis</i>).				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI TaxID=44161;				
RN	[1] - SEQUENCE FROM N.A. PubMed=8429550;	QY	7 ITLTPSSDVNTSEIYQVAPQYNNQALTAKYFQGAIDGSTLRFDPEKALQIANDIPOA 66		
RP	X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) MEDLINE=96211639; PubMed=8632451; DOI=10.1006/jmbi.1996.0152;	Db	31 IVLTPSSDLDNFNTVFPQQTINQALHLNAAQGADPLNLNFPEKALQIANGIPNS 90		
RX	Koni P.A., Ellar D.J.; "Cloning and characterization of a novel <i>Bacillus thuringiensis</i> cytolytic delta-endotoxin." J. Mol. Biol. 229:319-327(1993).	QY	67 AVNTLNQTVQQGTVQSYWIMDKIVDMDKVKLQDQVTAITNTFTNLNSQE 126		
RA	[2] X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) MEDLINE=96211639; PubMed=8632451; DOI=10.1006/jmbi.1996.0152;	Db	91 AIVTLNQSVIQTVESWMEQKQKIIQEVGLGVINSTSFMNSVEATIKGTFNLDTQI 150		
RA	Li J., Koni P.A., Ellar D.J.; "Structure of the mosquitoicid delta-endotoxin from <i>Bacillus thuringiensis</i> sp. <i>kyushuensis</i> and implications for membrane pore formation." J. Mol. Biol. 257:129-152(1996).	QY	127 SEAMPYKEDAKHTSYNNILFAQDEETGGWMLPPIAFDSVDIYQEVKLFVTIKDT 186		
RT	CC - FUNCTION: Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect midgut.	Db	151 DEAMFWHSLSAINTSYNNILSIQNETGAVMPLAEVSVDVEQKVLFFTIKDS 210		
RT	CC - SUBUNIT: Homodimer (protoxin) and monomer (active toxin).	QY	187 ENYAVTVAIINVYQALQSSRSKVYDAFK-SPRHLPRKRHKICSN 230		
RT	CC - DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	Db	211 ARYEVTKMKRALKTVQALHSS-NAPIVDIFVNNTYLYHSNHKITION 254		
RT	CC - PTM: Active after proteolytic processing.				
RT	CC - SIMILARITY: Belongs to the cyc1/cyc2 endotoxin family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).	RESULT 3			
CC	CC - DR: Z14147; CAA7519.1; -.	Q71KWB	PRELIMINARY; ID Q71KWB		
CC	CC - DR: S32432; S32432.	AC	Q71KWB; 27, Created)		
CC	CC - DR: 1CBY; X-ray; @=1-259.	DT	DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
CC	CC - DR: IPR001615; Endotoxin_CytB.	DT	DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
CC	CC - DR: PF01338; Bac_thur_toxin_1.	DB	Cytolytic delta-endotoxin.		
CC	CC - DR: ProDom; PD00944; Endotoxin_CytB; 1.	OS	<i>Bacillus thuringiensis</i> (subsp. <i>darmstadiensis</i>)		
CC	CC - DR: 3D-structure; Sporulation; Toxin.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> .		
CC	CC - DR: HELIX 51	RA	Promdonkoy B., Chuwawit N., Tanapongpipat S., Luxananil P., Pariyim S.;		
CC	CC - DR: HELIX 54	RA	"Cloning and characterization of a cytolytic and mosquito larvicidal delta-endotoxin from <i>Bacillus thuringiensis</i> subsp. <i>darmstadiensis</i> ." Curr. Microbiol. 46:94-98 (2003).		
CC	CC - DR: HELIX 63	RC	EMBL: AF072606; AM09651.1; -.		
CC	CC - DR: STRAND 68	DR	GO: 0005576; C: extracellular; IEA.		
CC	CC - DR: TURN 70	DR	GO: 0009405; P: spore wall assembly (sensu Bacteria); IEA.		
CC	CC - DR: TURN 75	DR	InterPro: IPR001615; Endotoxin_CytB.		
CC	CC - DR: TURN 84	DR	Pfam: Pf01338; Bac_thur_toxin_1.		
CC	CC - DR: TURN 86	DR	ProDom: PD00944; Endotoxin_CytB; 1.		
CC	CC - DR: TURN 88	SQ	SEQUENCE 259 AA: 29235 NW; 6924A01103D32B51 CRC64;		
CC	CC - DR: STRAND 68	QY	7 ITLTPSSDVNTSEIYQVAPQYNNQALTAKYFQGAIDGSTLRFDPEKALQIANDIPOA 66		
CC	CC - DR: TURN 72	Db	31 IVLTPSSDLDNFNTVFPQQTINQALHLNAAQGADPLNLNFPEKALQIANGIPNS 90		
CC	CC - DR: TURN 75	QY	67 AVNTLNQTVQQGTVQSYWIMDKIVDMDKVKLQDQVTAITNTFTNLNSQE 126		
CC	CC - DR: TURN 84	Db	91 AIVTLNQSVIQTVESWMEQKQKIIQEVGLGVINSTSFMNSVEATIKGTFNLDTQI 150		
CC	CC - DR: TURN 85	QY	127 SEAMPYKEDAKHTSYNNILFAQDEETGGWMLPPIAFDSVDIYQEVKLFVTIKDT 186		
CC	CC - DR: TURN 88	Db	151 DEAMFWHSLSAINTSYNNILSIQNETGAVMPLAEVSVDVEQKVLFFTIKDS 210		
CC	CC - DR: STRAND 68	QY	187 ENYAVTVAIINVYQALQSSRSKVYDAFK-SPRHLPRKRHKICSN 230		
CC	CC - DR: TURN 72	Db	211 ARYEVTKMKRALKTVQALHSS-NAPIVDIFVNNTYLYHSNHKITION 254		
CC	CC - DR: TURN 75				
CC	CC - DR: TURN 84				
CC	CC - DR: TURN 86				
CC	CC - DR: TURN 88				
CC	CC - DR: STRAND 68				
CC	CC - DR: TURN 72				
CC	CC - DR: TURN 75				
CC	CC - DR: TURN 84				
CC	CC - DR: TURN 86				
CC	CC - DR: TURN 88				
CC	CC - DR: STRAND 68				
CC	CC - DR: TURN 72				
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CC	CC - DR: TURN 88				
CC	CC - DR: STRAND 68				
CC	CC - DR: TURN 72				
CC	CC - DR: TURN 75				
CC	CC - DR: TURN 84				
CC	CC - DR: TURN 86				
CC	CC - DR: TURN 88				
CC	CC - DR: STRAND 68				
CC	CC - DR: TURN 72				
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CC	CC - DR: TURN 84				
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CC	CC - DR: STRAND 68				
CC	CC - DR: TURN 72				
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CC	CC - DR: STRAND 68				
CC	CC - DR: TURN 72				
CC	CC - DR: TURN 75				
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CC	CC - DR: STRAND 68				
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CC	CC - DR: TURN 86				
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CC	CC - DR: TURN 88				
CC	CC - DR: STRAND 68				
CC	CC - DR: TURN 72				
CC	CC - DR: TURN 75				
CC	CC - DR: TURN 84				
CC	CC - DR: TURN 86				
CC	CC - DR: TURN 88				
CC	CC - DR: STRAND 68				
CC	CC - DR: TURN 72				
CC	CC - DR: TURN 75				
CC	CC - DR: TURN 84				

RESULT 4						
Q8VNX0	PRELIMINARY;	PRT;	260	AA.		
ID						
AC						
DT	01-MAR-2002	(TREMBLref.)	20,	Created		
DT	01-MAR-2002	(TREMBLref.)	20,	Last sequence update		
DT	01-OCT-2003	(TREMBLref.)	25,	Last annotation update		
DE	Cyt2Bc Protein.					
GN	Name=cyt2Bc;					
OS	Bacillus thuringiensis (subsp. medellin)					
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.					
OX	NCBI_TaxID=79672;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE:21861241; PubMed=11872442;					
RX	DOI=10.1128/AEM.68.3.1228-1231.2002;					
RA	Juarez-Perez V., Guerchicoff A.; Rubinstein C., Delecluse A.;					
RT	"Characterization of Cyt2Bc toxin from Bacillus thuringiensis subsp. medellin."					
RT	medellin."					
RL	APPL Environ. Microbiol. 68:1228-1231(2002).					
DR	EMBL; AJ255979; CAC08987.1; -.					
DR	HSSP; Q04470; 1CYP.					
DR	GO; GO:0005576; C: extracellular; IFA.					
DR	GO; GO:000405; P: pathogenesis; IFA.					
DR	GO; GO:004243; P: spore wall assembly (sensu Bacteria); IFA.					
DR	Efam; PF011318; Bac thrus toxin; 1.					
DR	ProDom; PDO09844; Endoxocyt CytB; 1.					
DR	SEQUENCE 260 AA; 23716 MW; 8B87917B6FB485B4 CRC64;					
Query	RYITLTYPSSDVNVNSSEIYQVAQYVNNQALTAKYFGQAGDGSFLRFDFEKAQLQIANDIP	51.2%	Score 597;	DB 2;	Length 260;	
Best Local Similarity	52.9%	Pred. No. 3e-37;				
Matches	120;	Conservative	43;	Mismatches	62;	Indels 2; Gaps
DR	27 RHIATLIVSSDITNFNEFYYFVQYIAQRLRINTFQGAIDPLTNFNEKAQLQIANGIP					
DR	65 QPAAVVNTLNQTYQGQTGVQSYMMIDKIVDMKVNLSIVIDNKWFDQVTAIAITNTFTNLNS					
DR	87 NGAVGTGLNQSJTHQTIBSVMVISQKEIIRSVGLVINSANFWNNVVSATNTFTNLNP					
DR	125 QSEBAWPFYYKEDAHKTTSYYNLLPAIODEETGGVMTAPIADPSVIDEKVKLFVTIK					
DR	147 QVDENWIWNRNLSANQTSYYKLPISQKLPISQEDTGRFMAVLPIAEINVYHKKQQLFVTIK					
DR	185 DPENYATVKAIVNVQALQSSRSDSKVDAFKSPRHLPRKRHKICSN 230					
DR	207 DSARYEVKMKALTVVQAL-DSINAPILDVFNTHNSLHRPNTHILQN 252					

RESULT 5						
CYBA_BACTI	STANDARD;	PRT;	263	AA.		
ID	CYBA_BACTI					
AC	Q45723;					
DT	15-JUL-1998 (Rel. 36.	Created)				
DT	15-JUL-1998 (Rel. 36.	Last sequence update)				
DT	05-JUL-2004 (Rel. 44.	Last annotation update)				
DE	Type-2Ba cytolytic delta-endotoxin (29 kDa cytolytic toxin).					
GN	Name=cyt2B; Synonym=cyt2Ba7; CytB;					
OS	Bacillus thuringiensis (subsp. israelensis).					
OC	Plasmid pBR80.					
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.					
OX	NCBI_TaxID=1430;					
RN	SEQUENCE FROM N.A.					
RC	STRAIN=4Q2;					
RX	MEDLINE=97555937; PubMed=9212418;					
RA	Guerchicoff A., Ugale R.A., Rubinstein C.P.;					
RT	"Identification and characterization of a previously undescribed cyt					
RT	gene in Bacillus thuringiensis subsp. israelensis."					
RL	Appl. Environ. Microbiol. 63:216-217(1997).					
RN						

Page 4

- |- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
- |- PTM: Active after proteolytic processing (By similarity).
- |- SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.

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C EMBL: U82219; ARB93477.1; -
 R HSSP: Q04470; 1C8Y.
 R InterPro: IPR001615; Endotoxin_CytB.
 R Pfam: PF01338; Bac_thur_toxin_1.
 R ProDom: PD009844; Endotoxin_CytB_1.
 W Direct protein sequencing: Sporozoan Toxin.
 W SEQUENCE: 263 AA; 30059 MW; BDB7B2CDE690D9D CRC64;
 Q

```

Query Match      50.9%; Score 592.5; DB:1; Length 263;
Best Local Similarity 55.2%; Pred. No. 6.7e-37;
Matches 116; Conservative 40; Mismatches 53; Indels 1; Gaps 1;

```

5 RVIITLTVPSSDVNVNSSEIYQVAQVNNQALTLKRYFOGAGDSTLRFDFEKALQTANDIP 64
 6 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 27 RHITLTVPSSDLASFNTEFLYLEQQVAAQLRLNTFEQADPLTFLNFDFEKALQTANGLP 86

65 QAAVINTLNQTYQQGTYQVSYMDKIVDYMKNVLSIVIDNKKFWDQVTAITNTFTNLNS 124
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
87 NAGITGFLNQSITQOTIEISYMSQIKIIRNVYGLVINSTPNWSVLAAITNTFTNLNS 146

b	147	QVDENNTWVRNLNSATHTSYYKILFSIONEDTGFAMVLPIAFSLITDVQKQQLFFITR	206
y	125	QESEANITYYKTSYNNILFAIQDEETGGMATTPIAFDISVTEKEKYLFVTIK	184

RESULT 7
9L878 D Q9L878 PRELIMINARY; PRT; 263 AA.

C Q9L878; 01-OCT-2000 (TREMBLref. 15, Created)
 T 01-OCT-2000 (TREMBLref. 15, Last sequence update)
 T 01-OCT-2003 (TREMBLref. 25, Last annotation update)

E Cytolytic toxin Cyt2Ba8.
N Name=cyt2Ba8;
S Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

X X
N N
P P
C C
[1] SEQUENCE FROM N.A.
NCBI_TaxID=1428;
STRAIN=T36;

A Yu J., Pang Y.
A Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
R EMBL; AF215646; AAF37223.1; -.
R HSSP; Q04470; 1CBY.
R

Query Match	Score	DB 2	Length
Best Local Similarity	50.3%	Score 586; DB 2;	Length 263;
Probablility	52.0%	Pred. No. 2.1e-36;	-
SEQUENCE	263 AA:	29895 MW;	2

SU17 B
AA_BACTI
CXA_BACTI
PDB_2A5C
STANDARD; PRT; 249 AA.

pubmed; P0569; P0568; 13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)

Type-IAA Cytolytic derm-enocoxin (Z / Kd) cycloycic locin). Name-cyrlAA: Synonyms=cyclAA; *Bacillus thuringiensis* (subsp. *israelensis*), and *Bacillus thuringiensis* (subsp. *morrisonii*). Plasmid 72 v.

Fraxinus / A. Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1430, 1441; [1] SOURCE FROM N A

Species=Bacillus israelensis;
MEDLINE-B07085764; PubMed=3025452;
Ward B.S., Eber D.J.;
"Bacillus thuringiensis" var. *israelensis* delta-endotoxin. Nucleotide

sequence and characterization of the transcripts in *Bacillus thuringiensis* and *Escherichia coli*.ⁿ
J. Mol. Biol. 191:1-11(1996).
[2]

SEQUENCE FROM N.A.
SPECIES=*t. israelensis*;
MEDLINE=87085767; PubMed=3025453;
Ward E.S., Rdley A.R., Eltar D.J., Todd J.A.;

"Bacillus thuringiensis" var. *israelensis* delta-endotoxin. Cloning and expression of the toxin in sporogenic and asporogenic strains of *Bacillus subtilis*"; J. Mol. Biol. 191:13-22 (1986).

[3] SEQUENCE FROM N.A., AND MUTAGENESIS.
SPECIES=B.t.israelensis;
MEDLINE=89011977; PubMed=2845100.

Ward E.S., Ellar D.J., Chilcott C.N.; "Single amino acid changes in the *Bacillus thuringiensis* var. *israelensis* delta-endotoxin affect the toxicity and expression of the protein"; *J. Bact.* 172(11): 6627-6630.

J. Mol. Biol. 202:527-535 (1988).
 [4]
 SEQUENCE FROM N.A.
 SPECIES=B.t.israelensis;
 MOL wt=1050000;
 PROTEIN DOMAIN=DUTY;
 LIPOPROTEIN DOMAIN=DUTY.

MDBLNAME=806_221 ; FUDMEM=4U7003 ;
 Waaijwijk C., Dullmann A.M., van Wolkum M.E.S., Visser B.;
 "Molecular cloning and the nucleotide sequence of the Mr 28 000
 crystal protein gene of *Bacillus thuringiensis* subsp. *israelensis*.";
 Neth J Zool, 1991, 31, 101-105.

[5] Nucleic Acids Res. 13:620-621 (1985).
REVISIONS TO 34-35.
SPECIES=B.t. israelensis;
Waalwijk C.;
Submitted (FEB-1986) to the EMBL/GenBank/DDBJ databases.
[6]

RP	SEQUENCES FROM N.A.
RC	SPECIES=B. <i>t.</i> morrisoni; STRAIN=PG14;
RM	MEDLINE=8723386; PubMed=357510+;
RA	"Bacillus thuringiensis" var. <i>morrisoni</i> strain PG14: nucleotide sequence of gene encoding 27kDa crystal protein.";
RT	sequence of gene encoding 27kDa crystal protein.
RT	NUCLEIC ACIDS RES. 15:3619-3619(1987).
RL	[17]
RN	RP
RP	SEQUENCE FROM N.A.
RC	SPECIES=B. <i>t.</i> morrisoni; STRAIN=PG14;
RA	Gallart N.J., Sivasubramanian N., Federici B.A.; "Plasmid location, cloning, and sequence analysis of the gene encoding a 27-kilodalton cytolytic protein from <i>Bacillus thuringiensis</i> subsp. <i>morrisoni</i> (PG14)."; Curr. Microbiol. 16:171-177(1987).
CC	-PURPOSE: Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect midgut. Acts on mosquitoes and black flies.
CC	-DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC	-PIV: Active after proteolytic processing.
CC	-SIMILARITY: Belongs to the cyt/cyt endotoxin family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; X04338; CA27888.1; -
CC	DR EMBL; Y00132; CA26943.1; -
CC	DR EMBL; Y00135; CAAG8329.1; -
CC	DR EMBL; M35968; AA02553.1; -
CC	DR PIR; A24044; A24044.
CC	DR PIR; A27520; A27520.
CC	DR HSSP; Q04470; 1CBY.
CC	DR InterPro; IPR001615; Endotoxin_CytB.
CC	DR Pfam; PF01338; Bac_thur_toxin_1.
CC	DR ProDom; PD009844; Endotoxin_CytB.
KW	Plasmid; Sporulation; Toxin.
FT	VARIANT 82 82 P -> A (in strain Morrisoni).
SEQUENCE	249 AA; 27341 MW; E66194629D3989A CRC64;
Query Match	Score 39.1%; Length 249;
Best Local Similarity	45.6%; Pred. No. 1..3e-26;
Matches	99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;
Qy	5 RVIITTPPS-SDVVNTSEIYQV-APQYVNQNQALTAKYFQGAI-----DGSTLRFDFEKA 56
Db	25 RVITLRYDPNEINNLISINEIDNPNNYLQAIMLANAFQNALVPTSTDGFDALRFSMPKG 84
Qy	57 LQIANDI-PQAVVNTLQVTDKIVDKNVLSVYDQVTAI 115
Db	85 LEIANTITPMGAVVSYTDQVNTQTNQQSVMINKULEVLKTGVALSFSVT-DQLTAV 143
Qy	116 TNTFTNNSQSEAWIIFYKEDAHKTSYYNNILFAIQDETGGWMTPLIAFDISVIKE 175
Db	144 TNTFTNNTQRNBWIFWGKETANQNTYTNVLFQIAQNGQVGGVYCPVGFBIKVSAVK 203
Qy	176 EKVLFVTFIKDOPENYAVTKAANVVOQLQSSRSDSKVD 212
Db	204 EQVLFVTFIQDQSAYNTVNIQLKFAQPIVSSSQYPIAD 240
RESULT 9	
ID 052298	PRELIMINARY; PRT; 157 AA.
AC 052298	PRELIMINARY; PRT; 157 AA.
DT 01-JUN-1998	(TrEMBLrel. 06, Created)
DT 01-JUN-1998	(TrEMBLrel. 06, Last sequence update)
DR	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR	Cytolytic toxin (Fragment).
GN	Name=cyt2Ba;
OS	<i>Bacillus thuringiensis</i> (subsp. <i>tenebrionis</i>)
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> .
NCBI_TaxID	444;
OX	
RN	RP
RP	SEQUENCE FROM N.A.
RX	Medline=9755937; PubMed=9212418;
RA	Guerchicoff A., Ugaide R.A., Rubinstein C.P.;
RT	"Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> ."
RT	Appl. Environ. Microbiol. 63:2716-2721(1997).
RL	EMBL; AF039492.6; AACB5384.1; -.
DR	HSSP; Q04470; 1CBY.
DR	GO; GO:000576; C:extracellular; IEA.
DR	GO; GO:009405; P:spore wall assembly (sensu Bacteria); IEA.
DR	GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.
DR	InterPro; IPR001615; Endotoxin_CytB.
DR	Pfam; PF01338; Bac_thur_toxin_1.
DR	ProDom; PD009844; Endotoxin_CytB; 1.
FT	NON-TER 1 1
FT	NON-TER 157 157
FT	17716 MW; 7A00550DD3B8A124 CRC64;
SQ	SEQUENCE 157 AA; 17716 MW; 7A00550DD3B8A124 CRC64;
Query Match	Score 38.5%; Length 157;
Best Local Similarity	55.5%; Pred. No. 3e-26;
Matches	86; Conservative 32; Mismatches 37; Indels 0; Gaps 0;
Qy	40 FQGAIDGSTLRFDFEKAQIANDIPOAVVNTLNQGTYVQSVMDKUVDIMKVL 99
Db	3 FQGAIDPLTFLNFNEKAQLQANGLPNAQVTGTINQSVTHQTEVSVMSIQKEIIRSVLG 62
Qy	100 IVIDNCKFWQDVTAATNTFTNLSNSEAENTFYKEDAHKTSYYNNILFAIQDETGGV 159
Db	63 LVINSANFWNSVTAATNTFTNLEPVQDENWLVWRNLSATQTSYFKILFSIQNEDGRF 122
Qy	160 MATLPLTAFDISVIEKEKVLFLTIKDOPENYAVTK 194
Db	123 MAILPLAFeITVTDVQKQOLLPTITKIDSARYVKMK 157
RESULT 10	
ID Q7BVDA	PRELIMINARY; PRT; 157 AA.
ID Q7BVDA	PRELIMINARY; PRT; 157 AA.
AC	Q7BVDA; 1
DR	05-JUL-2004 (TrEMBLrel. 27, Created)
DR	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DR	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DR	Putative cytolytic toxin (Fragment).
OS	<i>Bacillus thuringiensis</i> .
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; <i>Bacillus</i> .
NCBI_TaxID	1428;
RN	SEQUENCE FROM N.A.
RC	Strain=4K3;
RX	Medline=9755937; PubMed=9212418;
RA	Guerchicoff A., Ugaide R.A., Rubinstein C.P.;
RT	"Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> ."
RT	Appl. Environ. Microbiol. 63:2716-2721(1997).
RL	EMBL; AF022886; AACB67600.1; -.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:009405; P:spore wall assembly (sensu Bacteria); IEA.
DR	InterPro; IPR001615; Endotoxin_CytB.
DR	Pfam; PF01338; Bac_thur_toxin_1.
DR	ProDom; PD009844; Endotoxin_CytB; 1.
FT	NON-TER 1 1
FT	NON-TER 157 157
FT	17716 MW; 7A00550DD3E8A124 CRC64;
SQ	SEQUENCE 157 AA; 17716 MW; 7A00550DD3E8A124 CRC64;
Query Match	Score 38.5%; Length 157;

Best Local Similarity 55.5%; Pred. No. 3e-26;	Matches 86; Conservative 32; Mismatches 37; Indels 0; Gaps 0;	OS Bacillus thuringiensis.
Matches 86; Conservative 32; Mismatches 37; Indels 0; Gaps 0;	OC Firmicutes; Bacillales; Bacillaceae; Bacillus.	
Qy 40 FGAGTDGSTRLDFEKAQIANDIPOAAVNTLNQTVQSVMDKIVDIMKNTLS 99	OC NCB_ TaxID=1428;	
Db 3 FGAGDPLTINFNFEKAQIANGLNAGTGTINSVHOTIEVSUMISIKEIIRSVLG 62	OC NCB_ TaxID=1428;	
Qy 100 IVIDNKKFWDQVTAATNTPTLNNSOEAWIIFYKKEDAHKTYYNNILFAIQDEETGGV 159	RN [1]	
Db 63 LVNSANFNSVVAATNTFTNLBODENWVNNSLATSQTSFYKILFSIONEDTGRF 122	RP SEQUENCE FROM N.A.	
Qy 160 MATLPIAFDISVDEKEKLFVTIKDTENYAV 194	RC STRAIN=4KL;	
Db 123 MAILPIAFETTDVQKQQLPITIKDSARVEVKMK 157	RC MEDLINE=9735537; PubMed=9212418;	
RESULT 11	RA Guerchicoff A., Ugale R.A., Rubinstein C.P.;	
ID O30895 PRELIMINARY; PRT; 156 AA.	RT "Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";	
AC 030895; PRT; 156 AA.	RT Appl. Environ. Microbiol. 63:2716-2721(1997).	
DT 01-JAN-1998 (TREMBLrel. 05, Created)	DR EMBL; AF022884; AAB87598; 1.	
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)	DR HSSP; Q04470; 1CBY.	
DE Cytolytic toxin homolog (Fragment).	DR GO; GO:0005576; C:extracellular; IEA.	
OS Bacillus thuringiensis (subsp. <i>israelensis</i>).	DR GO; GO:0009405; P:pathogen assembly; IEA.	
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.	
OX NCB_ TaxID=1430;	DR InterPro; IPR001615; Endotoxin_CytB.	
RN [1]	DR Pfam; PF01338; Bac_thur_toxin; 1.	
RP SEQUENCE FROM N.A.	DR ProDom; PD009844; Endotoxin_CytB; 1.	
RC STRAIN=9735537; PubMed=9212418;	FT NON TER 1	
RA Guerchicoff A., Ugale R.A., Rubinstein C.P.;	FT NON TER 156 AA; 17588 MW; 80550DD3E8A12413 CRC64;	
RT "Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";	FT SEQ 156 AA; 17588 MW; 80550DD3E8A12413 CRC64;	
RT Gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .	Query Match 38.0%; Score 443; DB 2; Length 156;	
DE Cytolytic toxin homolog (Fragment).	Best Local Similarity 55.9%; Pred. No. 7.e-26;	
OS Bacillus thuringiensis (subsp. <i>israelensis</i>).	Mismatches 31; Mismatches 36; Indels 0; Gaps 0;	
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	Matches 85; Conservative 31; Mismatches 36; Indels 0; Gaps 0;	
OX NCB_ TaxID=1430;	Query 40 FGAGTDGSTRLDFEKAQIANDIPOAAVNTLNQTVQSVMDKIVDIMKNTLS 99	
RN [1]	DB 3 FGAGDPLTINFNFEKAQIANGLNAGTGTINSVHOTIEVSUMISIKEIIRSVLG 62	
RP SEQUENCE FROM N.A.	Query 100 IVIDNKKFWDQVTAATNTPTLNNSQEAWIIFYKKEDAHKTYYNNILFAIQDEETGGV 159	
RC STRAIN=PG14;	DB 63 LVNSANFNSVVAATNTFTNLBODENWVNNSLATSQTSFYKILFSIONEDTGRF 122	
RA Guerchicoff A., Ugale R.A., Rubinstein C.P.;	Query 160 MATLPIAFDISVDEKEKLFVTIKDTENYAV 191	
RT "Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";	DB 123 MAILPIAFETTDVQKQQLPITIKDSARVEV 154	
RT Gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .	RESULT 13	
RT Appl. Environ. Microbiol. 63:2716-2721(1997).	ID O30969 PRELIMINARY; PRT; 156 AA.	
DR EMBL; AF022884; AAB87598; 1.	AC 030969; PRT; 156 AA.	
DR HSSP; Q04470; 1CBY.	AC 030969; PRELIMINARY; PRT; 156 AA.	
DR GO; GO:0009405; P:pathogen assembly; IEA.	AC 030969; PRELIMINARY; PRT; 156 AA.	
DR InterPro; IPR001615; Endotoxin_CytB.	AC 030969; PRELIMINARY; PRT; 156 AA.	
DR Pfam; PF01338; Bac_thur_toxin; 1.	AC 030969; PRELIMINARY; PRT; 156 AA.	
DR ProDom; PD009844; Endotoxin_CytB; 1.	AC 030969; PRELIMINARY; PRT; 156 AA.	
FT NON TER 1	AC 030969; PRELIMINARY; PRT; 156 AA.	
FT NON TER 156 AA; 17657 MW; 61440DD320A5C9 CRC64;	AC 030969; PRELIMINARY; PRT; 156 AA.	
FT SEQ 156 AA; 17657 MW; 61440DD320A5C9 CRC64;	AC 030969; PRELIMINARY; PRT; 156 AA.	
Query Match 38.1%; Score 444; DB 2; Length 156;	AC 030969; PRELIMINARY; PRT; 156 AA.	
Best Local Similarity 55.9%; Pred. No. 6.1e-26;	AC 030969; PRELIMINARY; PRT; 156 AA.	
Matches 85; Conservative 32; Mismatches 35; Indels 0; Gaps 0;	AC 030969; PRELIMINARY; PRT; 156 AA.	
Qy 40 FGAGTDGSTRLDFEKAQIANDIPOAAVNTLNQTVQSVMDKIVDIMKNTLS 99	DR SEQUENCE FROM N.A.	
Db 3 FGAGDPLTINFNFEKAQIANGLNAGTGTINSVHOTIEVSUMISIKEIIRSVLG 62	DR SEQUENCE FROM N.A.	
Qy 100 IVIDNKKFWDQVTAATNTPTLNNSOEAWIIFYKKEDAHKTYYNNILFAIQDEETGGV 159	RA MEDLINE=9735537; PubMed=9212418;	
Db 63 LVNSANFNSVVAATNTFTNLBODENWVNNSLATSQTSFYKILFSIONEDTGRF 122	RA Guerchicoff A., Ugale R.A., Rubinstein C.P.;	
Qy 160 MATLPIAFDISVDEKEKLFVTIKDTENYAV 191	RT "Identification and characterization of a previously undescribed cyt gene in <i>Bacillus thuringiensis</i> subsp. <i>israelensis</i> .";	
Db 123 MAILPIAFETTDVQKQQLPITIKDSARVEV 154	RT Appl. Environ. Microbiol. 63:2716-2721(1997).	
RESULT 12	DR EMBL; AF022884; AAB87598; 1.	
ID Q9R9C0 PRELIMINARY; PRT; 156 AA.	DR HSSP; Q04470; 1CBY.	
AC 09R9C0; PRT; 156 AA.	DR GO; GO:0005576; C:extracellular; IEA.	
DT 01-MAY-2000 (TREMBLrel. 13, Created)	DR GO; GO:0042243; P:spore wall assembly (sensu Bacteria); IEA.	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DR InterPro; IPR001615; Endotoxin_CytB.	
DE Putative cytolytic toxin (Fragment).	DR Pfam; PF01338; Bac_thur_toxin; 1.	
GN Name=cyt2Ba;	DR ProDom; PD009844; Endotoxin_CytB; 1.	
Query Match 37.9%; Score 442; DB 2; Length 156;	FT NON TER 1	
Best Local Similarity 55.3%; Pred. No. 8.6e-26;	FT SEQ 156 AA; 17574 MW; 80478F43E8A13B0C CRC64;	

Matches	84;	Conservative	32;	Mismatches	36;	Indels	0;	Gaps	0;	Db	215	DKRTVLPLTTDQYANYSNVIQTRFAQPLIDSRLAISNLSELRSSKYL	264
Qy	40	FOGAIDGSTLRLPDEKALQIANDIPQAVENTLNQTVQGTIVSYMDKIVDIMKRNQLS	99										
Db	3	FOGAIDPPTLNFNEKALQIANGIPNAQGTGTTINOSVTHOTIEVSMSIQKEIIRSTLG	62										
Qy	100	IVIDNKKFWDQVTAITFTNINQSSEAWIIFYKEDAHKTSYYNLFQATEETGCV	159										
Db	63	LVINSANTFNSVSAITFTNILEPQVTDENWVWRNLSATQTSYFKLFSIONEDGTF	122										
Qy	160	MATLPIAFADISVDIEKEKVLFVTIKDTENYAV	191										
Db	123	MATLPIAFELTVDWQKQQLFLITKDSARYEV	154										
RESULT 14													
CXBA_BACTW	ID_CXBA_BACTW	STANDARD;	PRT;	265	AA.					RN	[1]	SEQUENCE FROM N.A.	
AC	Q45790;									RP			
DR	15-JUL-1998	(Rel. 36, Created)								RC			
DR	15-JUL-1998	(Rel. 36, Last sequence update)								STRAIN=H30 / 163-131;			
DR	05-JUL-2004	(Rel. 44, Last annotation update)								MEDLINE=97176379; PubMed=9023925;			
DE	Type-1Ba	cycolytic delta-endotoxin.								Thiery L.; Delecluse A.; Tamayo M.C.; Ordzu S.;			
GN	Name=cyc1Ba1;									"Identifiensis" subsp. medellin and expression in a crystal-negative B.			
OS	Bacillus thuringiensis	(subsp. neoleoensis).								RT			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.									RT			
OX	NCBI_TaxID=43262;									RL			
RN	[1]									CC	-1-	FUNCTION: Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect midgut.	
RP	SEQUENCE FROM N.A.									CC	-1-	DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	
RC	SEQUINPS20116;									CC	-1-	SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.	
RA	Narva K.E.; Payne J.M.; Uyeda K.A.; Stalder C.J.; Michaels T.B.;									CC	-1-	PM: Active after proteolytic processing.	
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.									CC	-1-	PM: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-1-	FUNCTION: Kills the larvae of dipteran insects by making pores in the epithelial cell membrane of the insect midgut (By similarity).								CC	-1-	PM: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	
CC	-1-	DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.								CC	-1-	PM: This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-1-	SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.								CC	-1-	PM: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-1-	PM: Active after proteolytic processing (By similarity).								CC	-1-	PM: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	
CC	-1-	SIMILARITY: Belongs to the cyt1/cyt2 endotoxin family.								CC	-1-	PM: This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
DR	EMBL; AA03798; AA03693.1; -.									CC	-1-	PM: This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
DR	HSSP; Q04470; ICYB.									CC	-1-	PM: This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
DR	InterPro; IPR001615; Endotoxin_CytB.									CC	-1-	PM: This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
DR	PSM; P04470; Bac_thur_toxin_CytB.									CC	-1-	PM: This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
DR	ProDom; PDD09844; Endotoxin_CytB; 1.									CC	-1-	PM: This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
KW	Sporulation; Toxin.									CC	-1-	PM: This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
SQ	SEQUENCE 265 AA;	29906 MW;	260D1495F8C477A2	CRC64;						CC	-1-	PM: This statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
Query Match													
Best Local Similarity	36.4%	Score	423.5	DB 1;	Length	265;				Qy	54	KAQVAVNTLNQSEAWIIFYKEDAHKTSYYNLFQAIQDEBTGGWMATLPIAPDSV	112
Matches	94;	Conservative	47;	Mismatches	72;	Indels	17;	Gaps	6;	Db	83	TKGLEYANTISPQAVVYDQTLQSNNQVSYMDRVISVLTVMGVALSG-SITQTLTA	141
Qy	5	RTITLTIVPSSDVNVYSEIYVA-	---	POVNQALTLLARYFQGAI	---	DGSTLRFDFE	54			Qy	113	AAITNTFTNLSQSEAWIIFYKEDAHKTSYYNLFQAIQDEBTGGWMATLPIAPDSV	172
Db	38	RTIYKV--KDPIIDTQLEITEIENPVQVLAQAAFDQDLVPTETRCEAIRFMP	95							Db	142	SAVNTNTLNLTQKNEAWIIFYKEDAHKTSYYNLFQAIQDEBTGGWMATLPIAPDSV	201
Qy	55	KALQIANDI-PQAVAVNTLNQSEAWIIFYKEDAHKTSYYNLFQAIQDEBTGGWMATLPIAPDSV	113							Qy	173	IEKEKOLFLVFTIKDENTAVTKAINVVAQLOSSRDSKVD	212
Db	96	KGLEVAKTIQPKCAVWYDQTLQSNNQVSYMDRVISVLTVMGVALSG-SITQTLTA	154							Db	202	AVKERVFLFTIQDASVNTVQSLKFAQPLVSASEYPIAD	241
Qy	114	ATINTTPFLNQSSEAWIIFYKEDAHKTSYYNLFQAIQDEBTGGWMATLPIAPDSV	173							Qy	174	EKEKVLFLVFTIKDENTAVTKAINVVAQLOSSRDSKVD--AFKSPRHL	220
Db	155	ATDTDTFLNTQKDSANWFGETSHTQNTNTVNMFAIQNETTGRVMMCPGFEIRFT	214							Qy			
Qy												Search completed: June 26, 2005, 16:05:31	
												Job time : 177 sec	

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Result No.	Score	Query Match	Length DB	ID	Description
1	1165	100.0	231	14	US-10-386-972-2 Sequence 2, Appli
2	1165	100.0	231	14	US-10-386-972-2 Sequence 2, Appli
3	101	8.7	477	15	US-10-386-972-2 Sequence 9400, Ap
4	97	8.3	1833	8	US-08-945-567D-4 Sequence 4, Appli
5	97	8.3	1833	8	US-08-621-94JA-4 Sequence 4, Appli
6	97	8.3	1833	14	US-10-175-282-4 Sequence 4, Appli
7	97	8.3	1833	14	US-10-175-282-4 Sequence 4, Appli
8	97	8.3	1992	8	US-08-945-567D-3 Sequence 3, Appli
9	97	8.3	1992	8	US-08-621-94JA-3 Sequence 3, Appli
10	97	8.3	1992	14	US-10-175-282-3 Sequence 3, Appli
11	97	8.3	1992	14	US-10-175-275-3 Sequence 3, Appli

Qy 61 NDIPQAAVNTLNQTVQOGTVOVSVMIDKIVDKNVLSIVIDNKKFWDQVTAATNTFT 120
 Db 61 NDIPQAAVNTLNQTVQOGTVOVSVMIDKIVDKNVLSIVIDNKKFWDQVTAATNTFT 120
 Db 61 NDIPQAAVNTLNQTVQOGTVOVSVMIDKIVDKNVLSIVIDNKKFWDQVTAATNTFT 120
 Qy 121 NUNSQSEAWIIFYKEDAHKTSSYYNTLFAIODEETGGVMTPLIAFDISYDIEKEKVLF 180
 Db 121 NUNSQSEAWIIFYKEDAHKTSSYYNTLFAIODEETGGVMTPLIAFDISYDIEKEKVLF 180
 Qy 181 VTIKDENTAVTVKAINVQALLOSSRSKVDAFKSPRHLPRKRHKICNS 231
 Db 181 VTIKDENTAVTVKAINVQALLOSSRSKVDAFKSPRHLPRKRHKICNS 231

RESULT 2
 US-10-767-605-2
 / Sequence 2, Application US/10767605
 / Publication No. US20040127692A1
 / GENERAL INFORMATION:
 / APPLICANT: Rupar, Mark J.
 / APPLICANT: Donovan, William P.
 / APPLICANT: Tan, Yiping
 / APPLICANT: Sianey, Annette C.
 / TITLE OF INVENTION: Plants Toxic to Coleopteran Insects and Ctenocephalides spp.
 / FILE REFERENCE: MECO:017--3
 / CURRENT APPLICATION NUMBER: US/10/767,605
 / CURRENT FILING DATE: 2004-01-29
 / PRIOR APPLICATION NUMBER: 10/386,972
 / PRIOR FILING DATE: 2003-03-12
 / PRIOR APPLICATION NUMBER: 09/611,216
 / PRIOR FILING DATE: 2000-07-06
 / PRIOR APPLICATION NUMBER: 08/721,259
 / PRIOR FILING DATE: 1996-09-26
 / NUMBER OF SEQ ID NOS: 4
 / SEQ ID NO: 2
 / LENGTH: 231
 / TYPE: PRT
 / ORGANISM: *Bacillus thuringiensis*
 / US-10-767-605-2

Query Match 100.0%; Score 1165; DB 16; Length 231;
 Best Local Similarity 100.0%; Pred. No. 2.6e-99;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MFENRVTILTVSSDVNVNTSEIYQVQYNOQTLAKYFGAIDGSTLRDPFEQLQIA 60

Db 1 MFENRVTILTVSSDVNVNTSEIYQVQYNOQTLAKYFGAIDGSTLRDPFEQLQIA 60

Qy 61 NDIPQAAVNTLNQTVQOGTVOVSVMIDKIVDKNVLSIVIDNKKFWDQVTAATNTFT 120
 Db 61 NDIPQAAVNTLNQTVQOGTVOVSVMIDKIVDKNVLSIVIDNKKFWDQVTAATNTFT 120

Qy 121 NUNSQSEAWIIFYKEDAHKTSSYYNTLFAIODEETGGVMTPLIAFDISYDIEKEKVLF 180

Db 121 NUNSQSEAWIIFYKEDAHKTSSYYNTLFAIODEETGGVMTPLIAFDISYDIEKEKVLF 180

Qy 181 VTIKDENTAVTVKAINVQALLOSSRSKVDAFKSPRHLPRKRHKICNS 231
 Db 181 VTIKDENTAVTVKAINVQALLOSSRSKVDAFKSPRHLPRKRHKICNS 231

RESULT 3
 US-10-335-977-9400
 / Sequence 9400, Application US/10335977
 / Publication No. US20040052793A1
 / GENERAL INFORMATION:
 / APPLICANT: DOUGLAS SMITH et al
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 / RELATING TO HELICOBACTER PYLORI FOR
 / DIAGNOSTICS AND THERAPEUTICS
 / NUMBER OF SEQUENCES: 10031
 / CORRESPONDENCE ADDRESS:

RESULT 4
 US-08-945-567D-4
 / Sequence 4, Application US/08945567D
 / Publication No. US20010014672A1
 / GENERAL INFORMATION:
 / APPLICANT: SASAKI, Ken
 / APPLICANT: HARNES, Robin E.
 / APPLICANT: LOOSHORI, Sheena M.
 / APPLICANT: CHONG, Pele
 / APPLICANT: KLEIN, Michel H.
 / TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
 / MORAXELLA
 / FILE REFERENCE: 1038-745 MIS

CURRENT APPLICATION NUMBER: US/08/945,567D
 CURRENT FILING DATE: 1996-04-29
 PRIOR APPLICATION NUMBER: 08/431,718
 PRIOR FILING DATE: 1995-05-01
 PRIOR APPLICATION NUMBER: 08/478,370
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/621,944
 PRIOR FILING DATE: 1996-03-26
 PRIOR APPLICATION NUMBER: PCT/CA96/00264
 PRIOR FILING DATE: 1996-04-29
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 1833
 TYPE: PRT
 ORGANISM: Moraxella catarrhalis
 US-08-945-567D-4

Query Match 8.3%; Score 97; DB 8; Length 1833;
 Best Local Similarity 22.8%; Pred. No. 20; Mismatches 40; Indels 36; Gaps 7;
 Matches 50; Conservative 50; Mismatches 93; Indels 93; Gaps 93;

Qy 13 SSDVNVYSEIYQAPQVNQALTAKYFOGALDGSTLRFDFEKALQIAN-----61
 Db 898 SHDAVTGGKIVDLKTLENLKISSTAKTAQNSLHEPSVADEQNNFTVSNPYSSYDTSKTS 957

Qy 13 SSDVNVYSEIYQAPQVNQALTAKYFOGALDGSTLRFDFEKALQIAN-----61
 Db 898 SHDAVTGGKIVDLKTLENLKISSTAKTAQNSLHEPSVADEQNNFTVSNPYSSYDTSKTS 957

Qy 62 DIPQAAVNTLNQYQQCTVQYSVMDIKIVDIMK-----NVLSTIVDNKCFWDQVTAI 115
 Db 958 DVTFAGENGITTKVNGVVRGVIDQTPKLTVGNNNGKGIVIDSONGQNTIT-GL 1016

Qy 62 DIPQAAVNTLNQYQQCTVQYSVMDIKIVDIMK-----NVLSTIVDNKCFWDQVTAI 115
 Db 958 DVTFAGENGITTKVNGVVRGVIDQTPKLTVGNNNGKGIVIDSONGQNTIT-GL 1016

Qy 116 TNTFTNLNSQESAWIIFYKEDAHKTSYYNNILFAODEE---TGGWMATPLIAFDISVD 172
 Db 1017 SNTLANNTNDKGSV-----RTTEQGNI---IKDEDKTRAASIVDVLSSAGFNQGN 1063

Qy 173 IEKEKVLFVTKIDTENYAVTVKAINVQALOSSRDKV 211
 Db 1064 -GEAVDFVSTYDTVNFDLGNAATTAKYTYDDTSKTSKVKV 1100

RESULT 6
 US-10-175-282-4
 Sequence 4, Application US/10175282
 Publication No. US20030170657A1
 GENERAL INFORMATION:
 APPLICANT: SASAKI, Ken
 APPLICANT: HARNES, Robin E.
 APPLICANT: LOOSHORE, Sheena M.
 APPLICANT: CHONG, Peile
 APPLICANT: KLEIN, Michel H.
 TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
 FILE REFERENCE: MORAXELLA
 CURRENT APPLICATION NUMBER: US/10/175,282
 PRIOR APPLICATION NUMBER: 08/945,567
 PRIOR FILING DATE: 1998-03-19
 PRIOR APPLICATION NUMBER: 08/431,718
 PRIOR FILING DATE: 1995-05-01
 PRIOR APPLICATION NUMBER: 08/478,370
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/621,944
 PRIOR FILING DATE: 1996-03-26
 PRIOR APPLICATION NUMBER: PCT/CA96/00264
 NUMBER OF SEQ ID NOS: 10
 SEQ ID NO 4
 LENGTH: 1833
 TYPE: PRT
 ORGANISM: Moraxella catarrhalis
 US-10-175-282-4

Query Match 8.3%; Score 97; DB 14; Length 1833;
 Best Local Similarity 22.8%; Pred. No. 20; Mismatches 40; Indels 36; Gaps 7;
 Matches 50; Conservative 50; Mismatches 93; Indels 93; Gaps 93;

Qy 13 SSDVNVYSEIYQAPQVNQALTAKYFOGALDGSTLRFDFEKALQIAN-----61

Db 898 SHDAVTCGGKIVDLDKTELENKISSTAKTAQNSLHEFSVADEGNNFTVSNPYSSYDTSKS 957
 Qy 62 DIPQAAVNTLNQTVQGTTQVSIUMDKIVDIMK----NVLSVIDNKKFWDQVTAI 115
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 958 DVITFAGENGTTKVNKGVRGIDQTGGLTTPKLTVGNNNGKGIVIDSONGONTIT-GL 1016
 Qy 116 TNTFTNLNSQSEBAWIFYYKEADAHTSYNNILFAQDEB--TGGVMAATPLIAPDISVD 172
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 1017 SNTLANVNDGSV-----RTIEQNI--IKDEDTRAASIVDVLSAGFNQCN 1063
 Qy 173 IEKEKVLFVTIKDTEYAVTVKAIVNQALLOSSRDSKV 211
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 1064 -GEAVDFVSTYDTNFADGNATTAKTYDDTSKTSKV 1100

RESULT 7
 US-10-175-275-4
 ; Sequence 4, Application US/10175275
 ; Publication No. US20030171254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASAKI, Ken
 ; APPLICANT: HARNES, Robin E.
 ; APPLICANT: LOOSMORE, Sheena M.
 ; APPLICANT: CHONG, Pele
 ; APPLICANT: KLEIN, Michel H.
 ; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
 ; TITLE OF INVENTION: MORAXELLA
 ; FILE REFERENCE: 1038-745 MIS
 ; CURRENT APPLICATION NUMBER: US/08/945, 567D
 ; CURRENT FILING DATE: 1996-04-29
 ; PRIOR APPLICATION NUMBER: 08/431, 718
 ; PRIOR FILING DATE: 1995-05-01
 ; PRIOR APPLICATION NUMBER: 08/478, 370
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 08/621, 944
 ; PRIOR FILING DATE: 1996-03-26
 ; PRIOR APPLICATION NUMBER: PCT/CA96/00264
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1992
 ; TYPE: PRT
 ; ORGANISM: Moraxella catarrhalis
 ; US-08-945-567D-3

Query Match 8.3%; Score 97; DB 8; Length 1992;
 Best Local Similarity 22.8%; Pred. No. 23;
 Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;
 Gaps 7;

Qy 13 SSDVNVYSEIYQVAPQYVNNQALTARYFGQAAIDGSTLRFDEKALQAI-----61
 Db 1057 SHDAVTCGGKIVDLDKTELENKISSTAKTAQNSLHEFSVADEGNNFTVSNPYSSYDTSKS 1116
 Qy 62 DIPQAAVNTLNQTVQGTTQVSIUMDKIVDIMK----NVLSVIDNKKFWDQVTAI 115
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 1117 DVITPAGENGTTKVNKGVRGIDQTGGLTTPKLTVGNNNGKGIVIDSONGONTIT-GL 1175
 Qy 116 TNTFTNLNSQSEBAWIFYYKEADAHTSYNNILFAQDEB--TGGVMAATPLIAPDISVD 172
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 1176 SNTLLANVNDGSV-----RTIEQNI--IKDEDTRAASIVDVLSAGFNQCN 12224
 Qy 173 IEKEKVLFVTIKDTEYAVTVKAIVNQALLOSSRDSKV 211
 : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 Db 1223 -GEAVDFVSTYDTNFADGNATTAKTYDDTSKTSKV 1259

RESULT 9
 US-08-621-944A-3
 ; Sequence 3, Application US/08621944A
 ; Publication No. US20068070A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASAKI, Ken
 ; APPLICANT: HARNES, Robin E.
 ; APPLICANT: LOOSMORE, Sheena M.
 ; APPLICANT: KLEIN, Michel H.
 ; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sim & McBurney
 ; STREET: Suite 701, 310 University Avenue
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: MSG 1R7
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0., Version #1.30
 ; CURRENT APPLICATION DATA:
 ; RESULT 8
 ; US-08-945-567D-3
 ; Sequence 3, Application US/08945567D
 ; Publication No. US20010014672A1

APPLICATION NUMBER: US/08/621,944A
 FILING DATE: 26-MAR-1996
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/478,370
 FILING DATE: 07-JUN-1995
 CLASSIFICATION:
 NAME: Stewart, Michael I
 REFERENCE/DOCKET NUMBER: 24 ,373
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
 INFORMATION FOR SEQ ID NO: 3:
 SEQ ID NO: 3
 LENGTH: 1992 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-10-175-282-3

Query Match Score 97; DB 14; Length 1992;
 Best Local Similarity 22.8%; Pred. No. 23;
 Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

Qy 13 SSDVNYSEIYQAPQVNQALTAKYFGAIDGSTLRFDEKALQIAN----- 61
 Db 1057 SHDAVTGGKIVDLTKELENKISSTAKTAQNSLHEFSVDAEQNNFTVSNPSSYDTSKTS 1116
 Qy 62 DIPQAAVNTLNQTVQGTVQVSVMIDKIVDIMK-----NVLSIVIDNKKFDQVTAII 115
 Db 1117 DVITPAGENGITTKVNKGVRVGIDQTKGLTPKLTVGNNGKIVIDSQNGQTIT-GL 1175

Qy 116 TNTFTNLNSQSEAWIIFYKEDAHKTSTYYNLFIAQDEE---TGGYMATPLIAFDISVD 172
 Db 1176 SNTLANTVNDGSV-----RTEQGNI---IKDEDKTRAASIVDVLSAGFNQGN 1222

Qy 173 IEKEKVLFTIKTDENYAVTVKAINVVOALQSSRSKTV 211
 Db 1223 --GEAVDFVSTYDVTNFADGNATTAKTYDDTSKTSKTV 1259

RESULT 11
 US-10-175-275-3
 Sequence 3, Application US/10175275
 Publication No. US20030171254A1
 GENERAL INFORMATION:
 APPLICANT: SASAKI, Ken
 APPLICANT: HARKNESS, Robin E.
 APPLICANT: LOOSMORE, Sheena M.
 APPLICANT: CHONG, Pele
 APPLICANT: KLEIN, Michael H.
 TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
 TITLE OF INVENTION: MORAXELLA
 FILE REFERENCE: 1038-1235 MIS
 CURRENT APPLICATION NUMBER: US/10/175,275
 CURRENT FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: 08/945,567
 PRIOR FILING DATE: 1998-03-19
 PRIOR APPLICATION NUMBER: 08/431,718
 PRIOR FILING DATE: 1995-05-01
 PRIOR APPLICATION NUMBER: 08/478,370
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/621,944
 PRIOR FILING DATE: 1996-03-26
 PRIOR APPLICATION NUMBER: PCT/CA96/00264
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 1992
 TYPE: PRT
 ORGANISM: Moraxella catarrhalis
 US-10-175-275-3

RESULT 10
 US-10-175-202-3
 Sequence 3, Application US/10175282
 Publication No. US20030170657A1
 GENERAL INFORMATION:
 APPLICANT: SASAKI, Ken
 APPLICANT: HARKNESS, Robin E.
 APPLICANT: LOOSMORE, Sheena M.
 APPLICANT: CHONG, Pele
 APPLICANT: KLEIN, Michael H.
 TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
 TITLE OF INVENTION: MORAXELLA
 CURRENT APPLICATION NUMBER: US/10/175,282
 CURRENT FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: 08/945,567
 PRIOR FILING DATE: 1998-03-19
 PRIOR APPLICATION NUMBER: 08/431,718
 PRIOR FILING DATE: 1995-05-01
 PRIOR APPLICATION NUMBER: 08/478,370
 PRIOR FILING DATE: 1995-06-07
 PRIOR APPLICATION NUMBER: 08/621,944
 PRIOR FILING DATE: 1996-03-26
 PRIOR APPLICATION NUMBER: PCT/CA96/00264
 PRIOR FILING DATE: 1995-04-29
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 1992
 TYPE: PRT

Query Match Score 97; DB 14; Length 1992;
 Best Local Similarity 22.8%; Pred. No. 23;
 Matches 50; Conservative 40; Mismatches 93; Indels 36; Gaps 7;

Qy 13 SSDVNYSEIYQAPQVNQALTAKYFGAIDGSTLRFDEKALQIAN----- 61
 Db 1057 SHDAVTGGKIVDLTKELENKISSTAKTAQNSLHEFSVDAEQNNFTVSNPSSYDTSKTS 1116
 Qy 62 DIPQAAVNTLNQTVQGTVQVSVMIDKIVDIMK-----NVLSIVIDNKKFDQVTAII 115
 Db 1117 DVITPAGENGITTKVNKGVRVGIDQTKGLTPKLTVGNNGKIVIDSQNGQTIT-GL 1175

Qy 116 TNTFTNLNSQSEAWIIFYKEDAHKTSTYYNLFIAQDEE---TGGYMATPLIAFDISVD 172
 Db 1176 SNTLANTVNDGSV-----RTEQGNI---IKDEDKTRAASIVDVLSAGFNQGN 1222

Qy 173 I EKERVLPVTIKDENTAVTVKAINVQALLOSSRDKV 211
 Db 1223 - GRAFDPVSTDTNFDGNATTATYDTSKSKV 1259

RESULT 12
 US-10-282-122A-63417 ; Sequence 63417, Application US/10282122A
 ; Publication No. US20040029129A1
 / GENERAL INFORMATION:
 / APPLICANT: Wang, Liangbu
 / APPLICANT: Zamudio, Carlos
 / APPLICANT: Malone, Cheryl
 / APPLICANT: Ohlsen, Kari
 / APPLICANT: Zyskind, Judith
 / APPLICANT: Wall, Daniel
 / APPLICANT: Trawick, John
 / APPLICANT: Carr, Grant
 / APPLICANT: Yamamoto, Robert
 / APPLICANT: Forayth, R.
 / APPLICANT: Xu, H.
 / TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 / FILE REFERENCE: ELITRA.03A
 / CURRENT APPLICATION NUMBER: US/10/282,122A
 / CURRENT FILING DATE: 2003-02-20
 / PRIOR APPLICATION NUMBER: 60/191,078
 / PRIOR FILING DATE: 2000-03-21
 / PRIOR APPLICATION NUMBER: 60/206,848
 / PRIOR FILING DATE: 2000-05-23
 / PRIOR APPLICATION NUMBER: 60/207,727
 / PRIOR FILING DATE: 2000-05-26
 / PRIOR APPLICATION NUMBER: 60/230,335
 / PRIOR FILING DATE: 2000-09-06
 / PRIOR APPLICATION NUMBER: 60/230,347
 / PRIOR FILING DATE: 2000-09-16
 / PRIOR APPLICATION NUMBER: 60/230,347
 / PRIOR FILING DATE: 2000-09-09
 / PRIOR APPLICATION NUMBER: 60/242,578
 / PRIOR FILING DATE: 2000-10-23
 / PRIOR APPLICATION NUMBER: 60/253,625
 / PRIOR FILING DATE: 2000-11-27
 / PRIOR APPLICATION NUMBER: 60/257,931
 / PRIOR FILING DATE: 2000-12-22
 / PRIOR APPLICATION NUMBER: 60/267,636
 / PRIOR FILING DATE: 2001-02-09
 / PRIOR APPLICATION NUMBER: 60/269,308
 / PRIOR FILING DATE: 2001-02-16
 / NUMBER OF SEQ ID NOS: 78614
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 63417
 / LENGTH: 421
 / TYPE: PRT
 / ORGANISM: Mycoplasma genitalium
 US-10-282-122A-63417

Query Match 8.2%; Score 95.5; DB 15; Length 421;
 Best Local Similarity 23.6%; Pred. No. 3, 8; Gaps 8;
 Matches 41; Mismatches 75; Indels 39;

Qy 17 VNYSEIYQAPQQVNQALTLAKYFQGAIKGSTLRFDFEKALQIANDIPQAIVNTLNQTV 76
 Db 233 VKLSDMNQVLGRAVGNVYE---AV--NFLKQDLDQVCGQDFIDLMQTIVINTLERK 286

Qy 77 QGFTQVQSVMDKIVDIMKVNLSIVIDNKEFWDQTVAAITNTFTNLNSQSEAWIFFYKE 136
 Db 287 QAKTKQ----KAILEYQDVLT----SKKAWNREFSLFI-----BSQGENVELFTQKE 329

Qy 137 DAHKTSVYNNILFAIQDE:ETGVMMATPLIAPIA-DISVIEKEKV-----LEVTIK 184
 Db 330 GFFPKY---KASIKRAKSGSLHFTDPIDLAKIGINLGAGRMKCTTDQIDPMAGLFMCK 385

Qy 185 DTENYAVTVKAINVYORLQSSRD 207

RESULT 14
US-10-369-493-17326
Sequence 17326, Application US/10369493
GENERAL INFORMATION
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldmar, Barry S.
APPLICANT: Chen, Xianfang
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17326
LENGTH: 249
TYPE: PRT
ORGANISM: *Bacillus halodurans*
us-10-369-493-17326

Query Match 8.1%; Score 94.5; DB 15; Length 249;
Best Local Similarity 21.0%; Pred. No. 2,3; Mismatches 64; Indels 37; Gaps 7;
Matches 37; Conservative 38; Gapopen 115

Qy 62 DI PQA AVV NTI LQQT QO GTV QVS VMI ----- DKIV D MKVL SIV DN KKFWD QV TAI 115
Db 8 DV GKVR PHN ED NG TIME KQG LQV VAD GMGG HQ AGD VAS KMA TELL - KEAWE AS --- 62

Qy 116 TNT FTM NIS QSS A WTY KED DAH KT SY NTI LF A QD E B E T G V M A T L P I A F D I S V D E K 175
Db 63 --- LSP S Q OSE B G W L R N Q V L H N E S L Y H --- A Q H E E C G M G T T L --- V A A I V D K 109

Qy 176 EKV L F V T K D T E N Y A V T V K A I N V Q A L Q S S R D S K V D A F ----- K S P R H L P R K 223
Db 110 E R V T I A H G D S R A Y L I N E H G F S ----- Q K T R D H S L V N E L V R T G Q I S D E E A S H H P R K 160

RESULT 15
US-10-424-599-217207
Sequence 217207, Application US/10424599
GENERAL INFORMATION
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovacic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 217207
LENGTH: 356
TYPE: PRT
FEATURE: Glycine max
OTHER INFORMATION: Clone ID: PAT_MRT3847_38165C.1.pep

Query Match 8.1%; Score 94.5; DB 15; Length 356;
Best Local Similarity 20.7%; Pred. No. 3,7; Mismatches 39; Indels 69; Gaps 10;
Matches 58; Conservative 58; Gapopen 114;

Qy 5 R V I T L T V P S S D V ----- V Y T S E Y V Q V A P O Y V N Q A L T L A X Y F ----- 40
Db 74 R A L I T T A K N N I P W R K M A Q E I L E S V T R E L E S I Q N O S L V Y P D Y L N P H A Y E R G I N L T W L 133

RESULT 14
US-10-369-493-17326
Sequence 17326, Application US/10369493
GENERAL INFORMATION
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldmar, Barry S.
APPLICANT: Chen, Xianfang
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17326
LENGTH: 249
TYPE: PRT
ORGANISM: *Bacillus halodurans*
us-10-369-493-17326

Query Match 8.1%; Score 94.5; DB 15; Length 249;
Best Local Similarity 21.0%; Pred. No. 2,3; Mismatches 64; Indels 37; Gaps 7;
Matches 37; Conservative 38; Gapopen 115

Qy 41 --QGAGIDGSTL---RFDFEKALQIANDIPOAAVVNTLNQTVQGTVQVSVMIDKIVDIM 94
Db 134 AABEBAVATILMARRAPPDASSLQBANKILLGRNWLTANNHHMQ--YSESCVIDDIBI- 190

Qy 95 KNVLSIVIDNKKKFWDQV-TAAT-----NFTPNLNSQESE-----AWIFYKEDA- 138
Db 191 --GCSCVGISTRYLADKEPTAKTGFENISSYFVANNQOKQERAMPKEPKWTHANGEDPTV 248

Qy 139 --HKTSYYNILEPQDSET-----GGVMMATLPIAFDISVDEKEYLP 160
Db 249 LPSKSFDLVSIATFLHECPTRVIVNLVREAPRLRPCTLAFTDSLKSKVLOELSPVLF 308

Qy 181 VTIKDTERNYAVTVKAIVNVQALQS SRDSKVDAFKSPRHL 220

Db 309 TLVKS TBPF DLEYLTMDETIREAGFVNITSILTDPRHV 348

Search completed: June 26, 2005, 16:09:50
Job time : 160 secs

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Abu5493	Protein e					
Abu4537	Protein e					
Abu52293	Bacterial					
Abu53069	Protein					
Adb6078	Disease t					
Abu0784	Moraxella					
Aae0701	Moraxella					
Abu51662	Helicobac					
Abu49941	Protein e					
Aab69135	M. catarr					
Abm73470	Staphyloc					
Abz93309	A manganese					
Aay93312	A manganese					
Abu12072	Human NOV					
Adh72246	Human pro					
Abu50735	Helicobac					
Abu52262	Helicobac					
Abu25692	Protein e					
AdF07179	Bacterial					
Abu35493	Protein e					
26	95.5	8.2	421	6	ABU35493	
27	95.5	8.2	1876	6	Abu45937	
28	94.5	8.1	249	8	Adb52293	
29	94.5	8.1	393	6	Abu53069	
30	94.5	8.1	393	7	Adk6078	
31	93	8.0	2122	6	Abu0784	
32	93	8.0	2123	4	AAB0701	
33	92.5	7.9	1982	6	Abu51662	
34	92.5	7.9	4688	6	Abu49941	
35	92	7.9	2053	4	Aab69135	
36	90	7.7	293	6	Abm73470	
37	89.5	7.7	1059	3	AAY93309	
38	89.5	7.7	1084	3	AAY93312	
39	89.5	7.7	4903	6	Abu12072	
40	89.5	7.7	4913	8	ADH72246	
41	89.5	7.7	4961	8	ADH72236	
42	89	7.6	157	5	ABU50735	
43	89	7.6	182	5	ABU52262	
44	89	7.6	246	6	ABU25692	
45	89	7.6	373	7	ADF07179	

סימן יז

RESULT 1						
AAW55027	Minimum Match 0%	Maximum Match 100%	ID AAW55027 standard; protein; 231 AA.			
XX	Listing first 45 summaries					
database :	A_Geneseq_16Dec04:*					
1: geneseqD1980s:*						
2: geneseqD1990s:*						
3: geneseqD2000s:*						
4: geneseqD2010s:*						
5: geneseqD2002s:*						
6: geneseqD2003s:*						
7: geneseqD2003bs:*						
8: geneseqD2004s:*						
Bacillus thuringiensis	CryET29 protein.					
Bacillus thuringiensis	CryET29; crystal protein; Japanese beetle;					
Bacillus thuringiensis	Southern corn rootworm; Colorado potato beetle;					
KW	red flour beetle; cat flea; transgenic plant; insecticide.					
OS	Bacillus thuringiensis					
XX	WO9813497-A1.					
PN	WO9813497-A1.					
XX	02-APR-1998.					
PD	02-APR-1998.					
XX	PP 25-SEP-1997;					
PA	PP 25-SEP-1997;					
XX	PR 26-SEP-1996;					
XX	PR 26-SEP-1996;					
(ECOG-)	97WO-US017507.					
ECOGEN INC.	96US-00721259.					
Rubar MJ,	Tan Y,	Slaney AC;				
Donovan WP,						
XX	WPI; 1998-230707/20.					
DR	DR N-NSDB; AAV21172.					
XX	New Bacillus thuringiensis CryET29 crystal protein - having activity against e.g. Southern corn rootworm, Colorado potato beetle, Japanese beetle, red flour beetle and cat fleas.					
XX	Claim 2; Fig 1; 101pp; English.					
CC	The CryET29 crystal protein has activity against the Southern corn rootworm, Western corn rootworm, Colorado potato beetle, Japanese beetle and red flour beetle and also against fleas, in particular larvae of the cat fleas, Ctenocephalides felis. CryET29 can therefore be used to prevent infections by these insects. The gene can be used to produce transgenic plants which express the toxic proteins and therefor insecticidal activity against pests.					
CC	Sequence 231 AA;					
SQ	Query March 99 At: Score 1151: DR 2: Length 231					

Best Local Similarity 99.1%; Pred. No. 9.4e-104; Matches 229; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Db	85 LBIANTITPQGAVVSYVDQNVTQINQSVMINVKYLEVKLTVGLVALSGSVI -DQLTAAV 143
Qy 1 MFENRVTITLTPSSDVNVNQSEIYQVAPQQYNQALTLAKYFGAIDSTLRDFEKLQIA 60	Qy	116 INTFTNLNSQESENIFYKEDAHNTSYNNILPAIQDEETGGMNTLPIDFSDIEK 175
Db 1 MFENRVTITLTPSSDVNVNQSEIYQVAPQQYNQALTLAKYFGAIDSTLRDFEKLQIA 60	Db	144 TNTFTNLNTQNEAWIFWGETANTQNTYTNVLPAIQNAQTGGVNYCVPVGFELTKVSAVK 203
Qy 61 NDIPQAVAVNTLNQTYQGTQVQSYMDKIVDKNVLSIVIDNKFKMDFQVTAATNTFT 120	Qy	176 EKVLFTVTDKTENYAVTVAIINVYQALQSERDSKVVD 212
Db 61 NDIPQAVAVNTLNQTYQGTQVQSYMDKIVDKNVLSIVIDNKFKMDFQVTAATNTFT 120	Db	204 EQLEPTIQDQSNTVNQSLKFAQPLVSTQYPAD 240
Qy 121 NLNSQSEAWIIFYKEDAHNTSYNNILPAIQDEETGGMNTLPIDFSDIEKLV 180	RESULT 3	
Db 121 NLNSQSEAWIIFYKEDAHNTSYNNILPAIQDEETGGMNTLPIDFSDIEKLV 180	ID AAR04831	AAR04831 standard; protein; 249 AA.
Qy 181 VTIKDENTYAVTVKAINVQALQSSSDSKVDAFKSPRHLPKRHKICNS 231	XX	AC AAR04831;
Db 181 VTIKDENTYAVTVKAINVQALQSSSDSKVDAFKSPRHLPKRHKICNS 231	XX	DT 25-MAR-2003 (revised)
RESULT 2		
AAR10282	DE	Bacillus thuringiensis var. israelensis 27kd crystal protein.
ID AAR10282 standard; protein; 249 AA.	XX	Crystal protein; insecticide; Diptera.
XX	KW	
AC AAR10282;	XX	
XX	OS	Bacillus thuringiensis.
DT 04-APR-1991 (first entry)	XX	US4318006-A.
DB Mutant 27kd delta endotoxin.	XX	17-APR-1990.
XX	XX	PP 03-FEB-1986; 86US-00824912.
KW Mutant delta endotoxin; insecticide; mosquitos; chimeric protein.	XX	PR 01-JUL-1985; 85US-00750211.
XX	XX	(DUPO) DU PONT DB NEMOURS & CO E I.
OS Bacillus thuringiensis.	XX	PN US000875-H.
XX	PI	Ellar DJ, Ward ES;
PN US000875-H.	XX	WPI: 1990-156076/20.
PD 01-JAN-1991.	XX	DR N-PSDB; AAQ04456.
PF 18-MAR-1988; 88US-00170211.	XX	
PR 18-MAR-1988; 88US-00170211.	XX	
(DUPO) DU PONT DE NEMOURS & CO E I.	XX	Gene coding for Bacillus thuringiensis var israelensis crystal protein used to express insecticidal protein active esp. against order Diptera in larval form.
PI Ellar DJ, Ward ES;	XX	Disclosure; Page ?; -pp. English.
XX	PS	
DR WPI: 1991-028850/04.	XX	This is the sequence of a protein toxin with a mol.wt. of 27D which is homologous to the 26-280 protein present in crystal of B.thuringiensis var. israelensis. The protein is toxic to insect pests esp. Dipera (eg larvae of mosquitoes and blackflies) and used, either in its entirety or as an insecticidally effective fragment, as an insecticide. (Updated on 25-MAR-2003 to correct PA field.)
PT	XX	
CC This mutant 27 kd delta endotoxin has a single amino acid substitution (Arg 30 to Ala) in the wild-type sequence. This results in a soluble insecticidal protein with improved insecticidal properties - from Bacillus thuringiensis var. israelensis, have improved insecticidal properties, part. against mosquitoes.	XX	Query Match 39.1%; Score 456; DB 2; Length 249; Best Local Similarity 45.6%; Pred. No. 6.8e-36; Mismatches 44; Indels 10; Gaps 5; Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;
PS Disclosure; Fig 1; 14pp; English.	Db	57 LQIANDI-PQAIVVNTLNQTYQGTQVSYMDKIVDKNVLSIVIDNKFKMDFQVTAAI 115
XX	Qy	85 LEIANTITPQGAVVSYVDQNVTQINQSVMINVKYLEVKLTVGLVALSGSVI -DQLTAAV 143
CC This mutant 27 kd delta endotoxin has a single amino acid substitution (Arg 30 to Ala) in the wild-type sequence. This results in a soluble insecticidal protein with improved insecticidal properties - from Bacillus thuringiensis var. israelensis, have improved insecticidal properties, part. against mosquitoes.	Db	116 TNTFTNLNTQNEAWIFWGETANTQNTYTNVLPAIQNAQTGGVNYCVPVGFELTKVSAVK 203
CC haemolytic activity and greater expression in cells contg. sig. amts. of phosphatidate-type toxin receptors. It is hence useful e.g. against mosquitoes. See also AAR10283, AAR10283 and AAR10309	Qy	144 TNTFTNLNTQNEAWIFWGETANTQNTYTNVLPAIQNAQTGGVNYCVPVGFELTKVSAVK 203
XX	Db	176 EKVLFTVTDKTENYAVTVAIINVYQALQSSSRDKVVD 212
Sequence 249 AA;	Qy	
Query Match 39.2%; Score 457; DB 2; Length 249;	Db	5 RVITLTVPS-SDVNVNSEIYQV-APQYNNQALTLAKYFGQAI-----DGSTLRLDFEKA 56
Best Local Similarity 45.6%; Pred. No. 5.4e-16; Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;	Qy	57 RVITLTVPS-SDVNVNSEIYQV-APQYNNQALTLAKYFGQAI-----DGSTLRLDFEKA 56
CC 5 RVITLTVPS-SDVNVNSEIYQV-APQYNNQALTLAKYFGQAI-----DGSTLRLDFEKA 56	Db	25 RVITLVEDPNEINNLLSNEIDNPNTQALVPTSTDFDALRFSMPKG 84
PS 25 RVITLAVEDPNEINNLLSNEIDNPNTQALVPTSTDFDALRFSMPKG 84	Qy	57 LQIANDI-PQAIVVNTLNQTYQGTQVSYMDKIVDKNVLSIVIDNKFKMDFQVTAAI 115

Db	204 EQVLEFFTQDSASYNVNQLKEAQPVLSSQQPIAD	240	XX	04-APR-1991 (first entry)	
RESULT 4					
ID	AAR10853 standard; protein; 249 AA.	XX	DE	Mutant 27kD delta endotoxin.	
XX	AAR10853;	XX	XX	Mutant 27kD delta endotoxin; insecticide; mosquitoes; chimeric protein.	
AC		XX	KW	Bacillus thuringiensis.	
XX		XX	XX	Bacillus thuringiensis.	
DT	04-APR-1991 (first entry)	XX	XX		
XX		PD	01-JAN-1991.		
DE	Mutant 27kD delta endotoxin.	XX	XX		
XX	Mutant delta endotoxin; insecticide; mosquitoes; chimeric protein.	PP	18-MAR-1988;		
KW		XX	XX	88US-00170211.	
XX		PR	18-MAR-1988;		
OS	Bacillus thuringiensis.	PA	(DUPO) DU PONT DE NEMOURS & CO E I.		
XX		PA	XX		
PN	US000875-H.	PI	PI		
XX		Ellar DJ, Ward ES;	XX		
PD	01-JAN-1991.	XX	XX		
XX		DR	WPI; 1991-028850/04.		
PF	18-MAR-1988;	XX	XX		
XX	88US-00170211.	PT	Nucleic acid fragments encoding mutant 27 kD delta endotoxins - from		
PR	18-MAR-1988;	PT	Bacillus thuringiensis var. <i>Israelensis</i> , have improved insecticidal		
XX	88US-00170211.	PT	properties, part. against mosquitoes.		
PA	(DUPO) DU PONT DE NEMOURS & CO E I.	XX	XX		
XX		PS	Disclosure; Fig 1; 14pp; English.		
PI		XX	This mutant 27 kD delta endotoxin has a single amino acid substitution		
XX		XX	(Arg-78 to Ala) in the wild-type sequence. This results in a soluble		
DR	1991-028850/04.	XX	insecticidal protein with improved insecticidal properties, e.g. lower		
XX		PT	haemolytic activity and greater expression in cells contg. sig. amts. of		
PT	Nucleic acid fragments encoding mutant 27 kD delta endotoxins - from	CC	phosphatidate-type toxin receptors. It is hence useful e.g. against		
PT	Bacillus thuringiensis var. <i>Israelensis</i> , have improved insecticidal	CC	mosquitoes. See also AAR10853, AAR10282 and AAR10309		
PS	Properties, part. against mosquitoes.	XX	Sequence 249 AA;		
PS	PS Disclosure; Fig 1; 14pp; English.	XX	Query Match 38.6%; Score 450; DB 2; Length 249;		
XX	This mutant 27 kD delta endotoxin has a single amino acid substitution	CC	Best Local Similarity 45.2%; Pred. No. 2.6e-35;		
CC	(Arg-78 to Ala) in the wild-type sequence. This results in a soluble	CC	Matches 98; Conservative 44; Mismatches 65; Indels 10; Gaps 5;		
CC	insecticidal protein with improved insecticidal properties, e.g. lower	CC	Qy 5 RYITLTVPSSDVNVYNSBIQV-APOVNQALTAKYFQGAI-----DGSTARFDPEKA 56		
CC	haemolytic activity and greater expression in cells contg. sig. amts. of	CC	Db 25 RYITLRYEDPNEINNLISINEIDNPNPYILQAIMLANAFQNALVPTSTDFGDALAFSNMPKG 84		
CC	phosphatidate-type toxin receptors. It is hence useful e.g. against	XX	Qy 57 QIANDI-POAAVNTLNQTYQGQTQVSYMDKIVDIMKNVLSIVDNKKFWDQTAII 115		
CC	mosquitoes. See also AAR10282-83 and AAR10309	XX	Db 85 LBIANTITPMAVVSYTDQNTQTNNQSYVNTKVLRLTKTGVAVLSGSVT-DQTAIV 143		
XX	Sequence 249 AA;	XX	Qy 116 TNTPTNLNSQBSEAWIIFYKEDAHKTYYNLFIAQDEETCGVMATPLAPIFSDVIEK 175		
XX	Qy 6 VITLTVPSSDVNVYNSBIQV-APOVNQALTAKYFQGAI-----DGSTARFDPEKA 57	DB	Db 144 TNTPTNLNTQNEAWLFWKGKETANQTYNTVNLFAQNQATGQVMTCPVGPEIKVSASK 203		
Qy	VITLVEFPNEINNLISINEIDNPNPYILQAIMLANAFQNALVPTSTDFGDALAFSNMPKG 85	DB	Qy 176 EKVLFVTTIKDNTENAVTVKAINVVAQSLRSKVD 212		
Db	26 VITLVEFPNEINNLISINEIDNPNPYILQAIMLANAFQNALVPTSTDFGDALAFSNMPKG 85	DB	Db 204 EQVLEFFTQDSASYNVNQLKEAQPVLSSQQPIAD 240		
Qy	58 QIANDI-POAAVNTLNQTYQGQTQVSYMDKIVDIMKNVLSIVDNKKFWDQTAII 116	DB	RESULT 6		
Db	86 EITANTITPMAVVSYDQNTQTNNQSYVNTKVLRLTKTGVAVLSGSVT-DQTAIV 144	Db	AAR10309 standard; protein; 249 AA.		
Qy	117 NTPTNLNSQBSEAWIIFYKEDAHKTYYNLFIAQDEETCGVMATPLAPIFSDVIEK 176	XX	XX		
Db	145 NTPTNLNTQNEAWLFWKGKETANQTYNTVNLFAQNQATGQVMTCPVGPEIKVSASK 204	AC	AC AAR10309;		
Qy	177 KVLFVTTIKDNTENAVTVKAINVVAQSLRSKVD 212	XX	XX		
Db	205 QVLEFFTQDSASYNVNQLKEAQPVLSSQQPIAD 240	AC	04-APR-1991 (first entry)		
AC	AAR10283	XX	XX		
AC	AAR10283 standard; protein; 249 AA.	OS	Mutant 27kD delta endotoxin.		
AC	AAR10283	XX	OS	Bacillus thuringiensis.	
AC	AAR10283	XX	XX		

PN	US000875-H.	XX	XX	WPI; 1992-190107/23.
PD	01-JAN-1991.	XX	XX	Anticancer agent for thermo-chemotherapy - contains polypeptide produced from bacillus, and is pref. used with phloemycin.
PF	18-MAR-1988;	88US-00170211.	PT	PT
XX		XX	XX	
PR	18-MAR-1988;	88US-00170211.	PT	XX
XX		XX	XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E I.	XX	XX	Disclosure; Fig 1; spp; Japanese.
XX		XX	XX	
PI	Ellar DJ, Ward ES;	XX	XX	The sequence given is an anticancer agent for thermochemotherapy and has a molecular weight of 25000. This protein is very efficient esp. when used together with phloemycin and thermotherapy. This anticancer agent is pref. isolated from Bacillus thuringiensis
DR	WPI; 1991-028850/04.	XX	XX	
XX		XX	XX	
PS	Nucleic acid fragments encoding mutant 27 kD delta endotoxins - from Bacillus thuringiensis var. israelensis, have improved insecticidal properties, part. against mosquitoes.	XX	XX	Sequence 220 AA;
XX		XX	XX	
DISCLOSURE; Fig 1; 14pp; English.		XX	XX	
CC	This mutant 27 kD delta endotoxin has a single amino acid substitution (Lys-124 to Ala) in the wild-type sequence. This results in a soluble insecticidal protein with improved insecticidal properties, e.g. lower haemolytic activity and greater expression in cells contg. sig. amts. of phosphatidate-type toxin receptors. It is hence useful e.g. against mosquitoes. See also AARI0853 and AARI0282-83	CC	CC	
SQ	Sequence 249 AA;	CC	CC	
CC	Query Match 38.6%; Score 450;, DB 2; Length 249;	CC	CC	
CC	Best Local Similarity 45.2%; Pred. No. 2.6e-35;	CC	CC	
CC	Matches 98; Conservative 44; Mismatches 65; Indels 10; Gaps 5;	CC	CC	
Db	5 RVTILTVPS-S-DVNVYSEIYQV-APQVNQALTLAKYFOGAI-----DGSTLRFDFEKA 56	CC	CC	
Db	25 RVTILTVPS-EINNLISINEIDNPAYLQLRIMLANAFQNLAVPSTDFDALRSPMPKG 84	CC	CC	
CC	57 LQIANDI-PQAVVNTLNTQVQGTVQSVSMDKIVDIMKNVLSTIVDNRKFWDQVTAI 115	CC	CC	RESULT 8
Db	85 LEIANTITPMGAVVSTDQNVTQNNQSVWNINKLLEVATVLGALSIVI-DOLTAAV 143	CC	CC	AAP90062
CC	116 TNTFTNLSQSEAMWIPYKEDAHKTISYYNNILEAQDDETGGMATLPIAFDSDVIEK 175	CC	CC	ID AAP90062 standard; peptide; 218 AA.
Db	144 TNTFTNLTNTQNEAWIFWGKETANQNTNTVNLFAQNQAGTGGNYVCVPVGFEIKVSAYK 203	CC	CC	XX
CC	176 EKVLFVTTIKDOPENAVYTKAINVQALQSSDSKVVDD 212	CC	CC	AC AAP90062;
Db	204 EQVLFVTTIQDASAYNNVNIQSUKFAQPLVSSSTQYPIAD 240	CC	CC	XX
CC		CC	XX	DT 24-OCT-2003 (revised)
CC		CC	XX	DB 25-MAR-2003 (revised)
CC		CC	XX	DT 09-AUG-1990 (first entry)
CC		CC	XX	Peptide with anticancer activity.
CC		CC	XX	KW Anticancer agent; enhancer.
CC		CC	XX	Bacillus thuringiensis serovar israelensis; ONR-60A.
OS		XX	XX	OS
XX		XX	XX	XX
XX		XX	XX	PN JP01104019-A.
XX		XX	XX	XX
AC	AAR24023	XX	XX	PD 21-APR-1989.
XX		XX	XX	PF 29-JUL-1988;
DT	25-NOV-1992 (first entry)	XX	XX	PF 88JP-00188207.
XX		XX	XX	DE 31-JUL-1987;
DE	Anticancer agent.	XX	XX	PR 87JP-00180347.
XX		XX	XX	PA (TOAG) TOA GOSEI CHEM IND LTD.
KW	Thermochemotherapy; Bacillus thuringiensis.	XX	XX	XX
OS	Bacillus sp.	XX	XX	DR WPI; 1989-161673/22.
XX		XX	XX	XX
XX		XX	XX	Anticancer agents - contain polypeptide enhancer produced by Bacillus microorganism.
PN	JP04128240-A.	XX	XX	XX
XX		XX	XX	PS Claim 1; Fig 6; 7pp; Japanese.
PD	28-APR-1992.	XX	XX	XX
XX		XX	XX	CC The polypeptide has anticancer activity and is capable of synergistically enhancing other agents such as bisomycin, adriamycin, 5-FU and esp. CC neocarzinostatin and thio-TEP. See also J01104018. (Updated on 25-MAR- CC 2003 to correct PF field.) (Updated on 24-OCT-2003 to Standardise OS CC
PA	(TOAG) TOA GOSEI CHEM IND LTD.	XX	XX	

CC	field	XX	Sequence 265 AA;
SQ	Sequence 218 AA;	Query Match 36.4%; Score 424; DB 1; Length 218; Best Local Similarity 44.8%; Pred. No. 7.5e-33; Mismatches 90; Conservative 44; Gaps 5; Matches 57; Indels 10; Gaps 5;	Score 423.5; DB 2; Length 265; Best Local Similarity 40.9%; Pred. No. 1.1e-32; Mismatches 94; Conservative 47; Gaps 6; Matches 72; Indels 17; Gaps 6;
Qy	14 SDVNVNSRYYQV-APOVNQALTLAKYFQGAI-----DGSTLRFDBKALQJANDI-PQ 65	Qy 5 RVIITLTPSSDVNYSBIVQVA---PQVNQALTLAKYFQGAI-----DGSTLRFDFE 54	Qy 5 RVIITLTPSSDVNYSBIVQVA---PQVNQALTLAKYFQGAI-----DGSTLRFDFE 54
Db	6 NEINNLISINEIDNPNTLQAIMLANAFLQNALVPTSTDFGDALRFSMPKGLEJANTITPS 65	Db 38 RVIYKV--KDPDTQOLLETBENPNVYQAIQAAAQFDALVPTETEGEARFSMP 95	Db 38 RVIYKV--KDPDTQOLLETBENPNVYQAIQAAAQFDALVPTETEGEARFSMP 95
Qy	66 AAVVNTLNUQTVOGTGVNQVSMIDKIVDINKNLYSIVDNCKEFWDQVTAINTFTNLSQ 125	Qy 55 KALQIANDI-POAAVNTLNQTVQGTGVNQVSMIDKIVDINKNLYSIVDNCKEFWDQVTA 113	Qy 55 KALQIANDI-POAAVNTLNQTVQGTGVNQVSMIDKIVDINKNLYSIVDNCKEFWDQVTA 113
Db	66 GAVSVSYVHVTQTNN-QVSWMNKVLEVLKTVLGVALGSV1-DQLTAINTFTNLTQ 123	Db 96 KGLEVAKTIQPKGAVVAYTDQTLSQSNQVSVMDRVISVLKTVMGVALSG-SITQLTQ 154	Db 96 KGLEVAKTIQPKGAVVAYTDQTLSQSNQVSVMDRVISVLKTVMGVALSG-SITQLTQ 154
Qy	126 ESEAWIPIFYKEDAHKTSYYNNILFAIQDEETGSMATLPIAFDISYDIEKEKVLFTIKD 185	Qy 114 AITNTFVNQNEQESEAWIPIFYKEDAHKTSYYNNILFAIQDEETGSMATLPIAFDISYDIEKEKVLFTIKD 173	Qy 114 AITNTFVNQNEQESEAWIPIFYKEDAHKTSYYNNILFAIQDEETGSMATLPIAFDISYDIEKEKVLFTIKD 173
Db	124 KNEAWIPIFGKETANQNTNYVNLFAIQNAQTGGVMYCVPGFEIKYSAVEQVLFITIQD 183	Db 155 AITDIFTNLNFQDSAWVFMGKETSHQNTNYVNLFAIQNAQTGGVMYCVPGFEIKYSAVEQVLFITIQD 214	Db 155 AITDIFTNLNFQDSAWVFMGKETSHQNTNYVNLFAIQNAQTGGVMYCVPGFEIKYSAVEQVLFITIQD 214
Qy	186 TENAVTAKAINVQALQSSR 206	Qy 174 EKEKVLFTVKIDTENAVTAKAINVQALQSSRDSKVVD--AFKSPPRHL 220	Qy 174 EKEKVLFTVKIDTENAVTAKAINVQALQSSRDSKVVD--AFKSPPRHL 220
Db	184 SASYNNTNQSLKPAQPLVSSQ 204	Db 215 DKRTVILFLTTKDYANTSVNIGTLLRAQPLTDSRALAINDISEALRSSKYL 264	Db 215 DKRTVILFLTTKDYANTSVNIGTLLRAQPLTDSRALAINDISEALRSSKYL 264
<hr/>			
RESULT 9			
XX	XX	AAR91966 standard; protein; 265 AA.	AAR91966 standard; protein; 265 AA.
ID	XX	ID AAR91966	ID AAR91966
AC	XX	AC AAR91966;	AC AAR91966;
XX	XX	XX	XX
XX	XX	XX	XX
DT	16-OCT-2003 (revised)	DT 16-OCT-2003 (revised)	DT 16-OCT-2003 (revised)
DT	25-MAR-2003 (revised)	DT 25-MAR-2003 (revised)	DT 25-MAR-2003 (revised)
DT	15-AUG-1995 (first entry)	DT 18-JUL-1996 (first entry)	DT 18-JUL-1996 (first entry)
XX	XX	XX	XX
DB	Delta-endotoxin 201T6.	DE PS201T6 30 kDa toxin.	DE PS201T6 30 kDa toxin.
XX	XX	XX	XX
KW	Delta-endotoxin; crystal protein; insecticide; pesticide; biological control agent; pest control; yellow fever mosquito; Aedes aegypti; housefly; Musca domestica; leatmining fly; Liriomyza trifolii; Western corn rootworm; Diabrotica virgifera; dipteran insect.	Bacillus thuringiensis; isolate PS201T6.	Bacillus thuringiensis; isolate PS201T6.
OS	Bacillus thuringiensis; var. neoleoensis.	OS Bacillus thuringiensis; isolate PS201T6.	OS Bacillus thuringiensis; isolate PS201T6.
XX	XX	XX	XX
PN	W09502693-A1.	PP 30-SEP-1993; 93US-00129609.	PP 30-SEP-1993; 93US-00129609.
XX	XX	XX	XX
PD	26-JAN-1995.	PR 06-NOV-1991; 91US-00708654.	PR 06-NOV-1991; 91US-00708654.
XX	XX	PR 19-OCT-1992; 92US-00938551.	PR 19-OCT-1992; 92US-00938551.
PF	14-JUL-1994;	XX	XX
XX	94WO-US007887.	PA (MYCO) MYCOGEN CORP.	PA (MYCO) MYCOGEN CORP.
XX	XX	XX	XX
PR	15-JUL-1993; 93US-00093199.	PI Schnepf HE, Brower DO, Kennedy MK, Payne JM, Randall JB.	PI Schnepf HE, Brower DO, Kennedy MK, Payne JM, Randall JB.
PR	30-SEP-1993; 93US-00129650.	XX	XX
XX	XX	DR WPI; 1996-11559/12.	DR WPI; 1996-11559/12.
PA	(MYCO) MYCOGEN CORP.	XX	XX
XX	XX	DR N-PSDB; AAT16027.	DR N-PSDB; AAT16027.
PI	Payne J., Narva KB., Uyeda KA., Stalder CJ., Michaels TB;	PT New purified toxin active against cockroaches - produced by a culture of Bacillus thuringiensis isolate PS201T6, has a mol. wt. less than 31 kD.	PT New purified toxin active against cockroaches - produced by a culture of Bacillus thuringiensis isolate PS201T6, has a mol. wt. less than 31 kD.
XX	XX	XX	XX
DR	WPI: 1995-067337/09.	PS Example 3; Col 17-20; 12pp; English.	PS Example 3; Col 17-20; 12pp; English.
DR	DR N-PSDB; AA085261.	XX	XX
XX	XX	XX	XX
PT	Delta endotoxins produced by <i>Bacillus thuringiensis</i> isolates - are active against dipteran and/or corn rootworm.	CC This sequence represents the 30 kDa <i>Bacillus thuringiensis</i> (B.t.) toxin, which is active against cockroaches. The encoding sequence was obtained CC from the B.t. isolate P201T6, using the primers represented by AAT16031 CC and AAT16032. The toxin has a high activity against cockroaches while CC not affecting humans or animals. Insecticides such as this can be safely CC used in homes and restaurants. These insecticides will also be effective CC against strains resistant to currently used insecticides. The B.t. CC isolate PS201T6 may also be used directly to control the cockroaches. CC (Updated on 25-MAR-2003 to correct PP field.) (Updated on 16-OCT-2003 to CC standardise OS field)	CC This sequence represents the 30 kDa <i>Bacillus thuringiensis</i> (B.t.) toxin, which is active against cockroaches. The encoding sequence was obtained CC from the B.t. isolate P201T6, using the primers represented by AAT16031 CC and AAT16032. The toxin has a high activity against cockroaches while CC not affecting humans or animals. Insecticides such as this can be safely CC used in homes and restaurants. These insecticides will also be effective CC against strains resistant to currently used insecticides. The B.t. CC isolate PS201T6 may also be used directly to control the cockroaches. CC (Updated on 25-MAR-2003 to correct PP field.) (Updated on 16-OCT-2003 to CC standardise OS field)
PS	PS	XX	XX
PS	Page 32-33; 38pp; English.	XX	XX
PS	PS encoding a novel 30 kDa delta-endotoxin, 201T6 toxin, was isolated from a gene library of <i>Bacillus thuringiensis</i> PS001T6 (NRRL B-18750) in Lambda Gem-11. Removal of the 43 N-terminal amino acids of the toxin gave a 27 kDa toxin (AAR7055) of increased scope and potency. Recombinant hosts expressing the toxin gene are used for biological control of insect pests. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)	CC This sequence represents the 30 kDa <i>Bacillus thuringiensis</i> (B.t.) toxin, which is active against cockroaches. The encoding sequence was obtained CC from the B.t. isolate P201T6, using the primers represented by AAT16031 CC and AAT16032. The toxin has a high activity against cockroaches while CC not affecting humans or animals. Insecticides such as this can be safely CC used in homes and restaurants. These insecticides will also be effective CC against strains resistant to currently used insecticides. The B.t. CC isolate PS201T6 may also be used directly to control the cockroaches. CC (Updated on 25-MAR-2003 to correct PP field.) (Updated on 16-OCT-2003 to CC standardise OS field)	CC This sequence represents the 30 kDa <i>Bacillus thuringiensis</i> (B.t.) toxin, which is active against cockroaches. The encoding sequence was obtained CC from the B.t. isolate P201T6, using the primers represented by AAT16031 CC and AAT16032. The toxin has a high activity against cockroaches while CC not affecting humans or animals. Insecticides such as this can be safely CC used in homes and restaurants. These insecticides will also be effective CC against strains resistant to currently used insecticides. The B.t. CC isolate PS201T6 may also be used directly to control the cockroaches. CC (Updated on 25-MAR-2003 to correct PP field.) (Updated on 16-OCT-2003 to CC standardise OS field)
PS	PS	XX	XX

Query Match 36.4%; Score 423.5; DB 2; Length 265;
 Best Local Similarity 40.9%; Pred. No. 1.1e-32;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVIITLVPSDVNYSEIYQVA---PQYUNQALITAKEYFGQAI---DGSTLRFDPB 54
 Db 38 RVIYKV--KOPIDTQOLETEIENPVYVQAIQIAAFQDALYETETEFGEARTRFSMP 95

Qy 55 KALQIANDI-I-POAATVNTLNQTVQGTRVQVSVMIDKIVDINKVNTSIVIDNKRPEVDQVTA 113
 Db 96 KGLEVAKTIQPKGAVVAYTQDTLSQSNNQVSUMIDRVISVLTQNGVALSG-SITQLTA 154

Qy 114 AITNTFTNLNSOEEAWEIIFTYKEDAHKTSTYYNILPAIDQDEETGGYMATPLPIAFDISVDI 173
 Db 155 AITDTFTNLNFORTDSAWFVWGETSHOTNTYVNMFAQNTEGTMCMVPIGFELRVPFT 214

Qy 174 EKEKVLFLVTKDENTAVTKAINVYQALQSSRDSEKVD---AFKSPPRL 220
 Db 215 DKRTVLFLLTDKDYANTSVNIGTQRLFAQPLIDSRLSINDLSEALRSSKYL 264

RESULT 11
 AA0W850 ID AA0W850 standard; protein; 265 AA.

XX AC AA0W850;
 XX DT 17-OCT-2003 (revised)
 DT 27-AUG-1997 (first entry)
 XX DB Delta-endotoxin.
 XX Delta-endotoxin; *Bacillus thuringiensis*; Gram-positive bacteria; mirid; -kw spore forming bacteria; parasporal crystalline protein; *Lygus hesperus*; hemipreren insect; insect pest; crop pest; leaf bug; *Lygus lineolaris*; pesticide.
 XX OS *Bacillus thuringiensis*; strain PS201T6.
 XX FH Location/Qualifiers
 FT Misc-difference 1 .43
 FT /note= "removed to create activated truncated endotoxin"
 Protein 44. .265
 FT /note= "mature activated delta-endotoxin"
 XX PN WO9639843-A1.
 XX PD 19-DEC-1996.
 XX PF 07-JUN-1996; 96WO-US009987.
 PR 07-JUN-1995; 95US-00475924.
 PA (MYCO) MYCOGEN CORP.
 PI Stockhoff B, Conlan C;
 XX DR WPI; 1997-051641/05.
 DR N-PSDB; AAT47253.
 XX PT Biological control of hemipteran insect pests - using *Bacillus thuringiensis* delta-endotoxin, pref. expressed by transformed plants.
 XX PS Disclosure; Page 19-20; 28pp; English.

This sequence represents the delta-endotoxin of *Bacillus thuringiensis* (B.t.) isolate PS201T6. B.t. is a gram-positive, spore forming bacterium characterised by parasporal crystalline protein inclusions. The proteins can be highly toxic to pests and are specific in their toxic activity, and include the delta-endotoxins. The crystalline toxins are generally recognised as being protoxins, requiring either particular physiochemical conditions or the action of certain proteases to generate an active toxin. This protein sequence is activated by the removal of 43 N-terminal amino acids. The protein can be used in the method of the invention. The method of the invention is for controlling hemipteran insect pests. The method comprises the administration of a B.. delta-endotoxin to the pests or their environment. Of the hemipteran insect pests, the mirids (including Lygus) are the most notorious crop pests. The endotoxin encoded by this sequence is especially useful for controlling the leaf bugs *Lygus hesperus* and *L. lineolaris*. The method provides an environmentally acceptable alternative to the use of chemical pesticides. (updated on 17-OCT-2003 to standardise OS field)

Sequence 265 AA;

Query Match 36.4%; Score 423.5; DB 2; Length 265;
 Best Local Similarity 40.9%; Pred. No. 1.1e-32;
 Matches 94; Conservative 47; Mismatches 72; Indels 17; Gaps 6;

Qy 5 RVIITLVPSDVNYSEIYQVA---PQYUNQALITAKEYFGQAI---DGSTLRFDPB 54
 Db 38 RVIYKV--KOPIDTQOLETEIENPVYVQAIQIAAFQDALYETETEFGEARTRFSMP 95

Qy 55 KALQIANDI-I-POAATVNTLNQTVQGTRVQVSVMKIVDINKVNTSIVIDNKKPFDQVTA 113
 Db 96 KGLEVAKTIQPKGAVVAYTQDTLSQSNNQVSUMIDRVISVLTQNGVALSG-SITQLTA 154

Qy 114 AITNTFTNLNSOEEAWEIIFTYKEDAHKTSTYYNILPAIDQDEETGGYMATPLPIAFDISVDI 173
 Db 155 AITDTFTNLNFORTDSAWFVWGETSHOTNTYVNMFAQNTEGTMCMVPIGFELRVPFT 214

Qy 174 EKEKVLFLVTKDENTAVTKAINVYQALQSSRDSEKVD---AFKSPPRL 220
 Db 215 DKRTVLFLLTDKDYANTSVNIGTQRLFAQPLIDSRLSINDLSEALRSSKYL 264

RESULT 12
 AAY01207
 ID AAY01207 standard; protein; 265 AA.

XX AC AAY01207;
 XX DT 20-MAR-2003 (revised)
 DT 25-MAY-1999 (first entry)
 XX DB *B. thuringiensis* PS201T6 30kD delta-endotoxin.
 XX KW Hemipteran; insect; pest; *Bacillus thuringiensis*; delta-endotoxin; Lygus hesperus; *Lycus lineolaris*; insecticide; chemical pesticide; insect management; insecticide resistance.
 XX OS *Bacillus thuringiensis*.
 XX PN US5885963-A.
 XX PR 07-JUN-1995; 95US-00657579.
 XX PD 23-MAR-1999.
 XX PP 07-JUN-1996; 96US-00657579.
 XX PR 07-JUN-1995; 95US-00475924.
 XX PA (MYCO) MYCOGEN CORP.
 XX PI Conlan C, Stockhoff B;
 XX DR WPI; 1999-2288382/19.
 XX DR N-PSDB; AAX26394.

New method of killing hemipteran insect pests - by administration of a *Bacillus thuringiensis* delta-endotoxin from the *B. thuringiensis* isolate PS1201, deposited in NRRL B-21011.

Example; Col 15-16; 10pp; English.

The invention relates to killing hemipteran insect pests by administering

a *Bacillus thuringiensis* delta-endotoxin from *B. thuringiensis* isolate PS123D1, deposited in NRRL B-21011. The hemipteran insect pests that can be controlled by the method are specifically Lygus hesperus and Lygus lineolaris. The method provides an alternative to control of hemipteran pests with chemical pesticides, allowing more environmental friendly insect management and provides a tool for management of insecticide resistance. The present sequence represents an approximately 30kD delta-endotoxin of *B. thuringiensis* isolate PS201T6. (Updated on 20-MAR-2003 to correct PP field.)

XX

Sequence 265 AA;

Query Match	36.4%	Score	423.5;	DB	2;	Length	265;
Best Local Similarity	40.9%	Pred.	No. 1.1e-32;				
Matches	94;	Conservative	47;	Mismatches	72;	Indels	17;
						Gap*	6;

Qy 5 RVIITLVPSSDPVNVSEIYQVA---POVNQNLTLAKYFOGAI----DGSTLRFPEKALQIANDI-PQA 66
 Db 38 RVIYLKV-KDPIDTTQLEITBTRIENPVLVQLQIOLAFAQDALVPTEFGBAIRFSMP 95
 Qy 55 KALQIANDI-PQAVAVNTLNQTVQGGTVQVSWMIDKTVUDIMKVNLSIVIDNKKFWDQVTA 113
 Db 96 KGLEVAKTIQPKGAVVAYTDQTSQSNNQVSWMIDRVTSVLLKTMGV/ALSG-SITPOLTA 154
 Qy 114 AITDTFTNLNSOSEANFPPYKEEDAHKTYYNNILFAQDEETGGMNLPIAFDISVDI 173
 Db 155 AITDTFTNLNTQKDSAWFWGETSHQNYTNVMFAQNETGRVMCVPGFERKVFT 214
 Qy 174 EKEKVLFTTIKOTENYATVKAINVQVQLQSSRDSKVVD---AFKSPRHL 220
 Db 215 DKEKVLFTTIKOTDQANYSYNSNIQTURFAQPLIDSRLSALNSINDLSEALRSSKL 264

RESULT 13

AAR70755

ID AAR70755 standard; protein; 222 AA.

XX

AC AAR91967;

XX

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 15-AUG-1995 (first entry)

XX

DE Delta-endotoxin 201T6 truncation.

XX

KW Delta-endotoxin; crystal protein; insecticide; pesticide;

KW biological control agent; pest control; yellow fever mosquito;

KW Aedes aegypti; housefly; Musca domestica; leafmining fly;

KW Liriomyza trifolioli; Western corn rootworm; Diabrotica virgifera;

KW dipteran insect.

XX

OS *Bacillus thuringiensis*; var. *neoleoensis*.

XX

W09502693-A1.

XX

PD 26-JAN-1995.

XX

PP 14-JUL-1994; 94WO-US007887.

PN 15-JUL-1993; 93US-00093199.

PR 30-SEP-1993; 93US-00129610.

PA (MYCO) MYCOGEN CORP.

XX

PP Payne J, Narva KE, Uyeda KA, Staider CJ, Michaels TE;

XX

DR WPI; 1995-067337/09.

DR N-PSDB; AAQ85261.

XX

PT Delta endotoxins produced by *Bacillus thuringiensis* isolates - are active

PT against dipteran and/or corn rootworm.

XX

PS Claim 5; Page 33-34; 38pp; English.

XX

DNA encoding a novel 30 kDa delta-endotoxin, 201T6 toxin, was isolated from a gene library of *Bacillus thuringiensis* PS01T6 (NRRL B-18750) in lambda Gem-11. Removal of the 43 N-terminal amino acids of the toxin gave a 25 kD toxin (AAR70755) of increased scope and potency. Recombinant hosts expressing the toxin gene are used for biological control of insect pests. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)

XX

SQ Sequence 222 AA;

XX

Query

Match

35.8%

Score

417;

DB

2;

Length

222;

;

Best

Local

Similarity

41.9%

Pred.

No.

3.7e-32;

;

Matches

91;

Conservative

42;

Mismatches

72;

Indels

12;

Gaps

5;

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toxin has a high activity against cockroaches, while not affecting humans or animals. Insecticides such as this can be safely used in homes and restaurants. These insecticides will also be effective against strains resistant to currently used insecticides. The B.t. isolate PS201T6 may also be used directly to control the cockroaches. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field)

Sequence 222 AA;

```
Query Match 35.8%; Score 417; DB 2; Length 222;
Best Local Similarity 41.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;
Qy      15 DVVNYSEIXOVA-POVNQNLTLAKYFOGAI-----DGSTLRFDFEKAQIANDI-PQA 66
Db       6 DTTQLEITEENPVLYQLQIAQDAAFDALVPTEFGFAIRFSMPKGLEVAKTIQPKG 65
Qy      67 AVNTLNQTYQOGTQVSMSMIDKIVDMMKVLSTIVDNKKFWQVTAATNTFTNLSQE 126
Db       66 AVVAYTDQTLSQSNQQSVMSMDRVTSVLIKTVMGVLSSG-SITQQTAAATDTFTNLTQK 124
Qy      127 SEAWIIFYKEDAHKSYYYNNILFALQDEETGGVNMATLPIAFDISYDIEKEKVLFTIKDT 186
Db       125 DSAWFWGKETSHQNYTNVMFAQNETIGRVMCVPGEIRVFTDKRTVLFLITKDY 184
Qy      187 ENYAVTVKAINVQALQSRSDSKVVD--AFKSPPHL 220
Db       185 ANYSYNIQTLRFAQPLIDSRLSINDLSEALRSSKYL 221
```

RESULT 15
ID AAY01208 Standard: protein; 222 AA.
XX AAY01208;
.AC
XX DT 20-MAR-2003 (revised)
XX 25-MAY-1999 (first entry)

DB. thuringiensis PS201T6 truncated delta-endotoxin.
KW Hemipteran; insect; pest; Bacillus thuringiensis; delta-endotoxin;
KW Lygus hesperus; Lygus lineolaris; insecticide; chemical pesticide;
XX insect management; insecticide resistance.
OS Bacillus thuringiensis.

PN US5885963-A.
XX 23-MAR-1999.
PD XX
XX PP 07-JUN-1996; 96US-00657579.
XX PR 07-JUN-1995; 95US-00475924.
XX PA (MYCO) MYCOGEN CORP.
XX PI Conlan C, Stockhoff B;
XX DR WPI; 1999-228582/19.

XX New method of killing hemipteran insect pests - by administration of a
PT Bacillus thuringiensis delta-endotoxin from B. thuringiensis isolate
PT PS123D1, deposited in NBRRL B-21011. The hemipteran insect pests that can
XX be controlled by the method are specifically Lygus hesperus and Lygus
CC lineolaris. The method provides an alternative to control of hemipteran
CC pests with chemical pesticides, allowing more environmentally-friendly
CC

insect management and provides a tool for management of insecticide
resistance. The present sequence represents a truncated delta-endotoxin
of B. thuringiensis isolate PS201T6 of about 25 kD. (Updated on 20-MAR-
2003 to correct PF field.)

Sequence 222 AA;

```
Query Match 35.8%; Score 417; DB 2; Length 222;
Best Local Similarity 41.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;
Qy      15 DVVNYSEIXOVA-POVNQNLTLAKYFOGAI-----DGSTLRFDFEKAQIANDI-PQA 66
Db       6 DTTQLEITEENPVLYQLQIAQDAAFDALVPTEFGFAIRFSMPKGLEVAKTIQPKG 65
Qy      67 AVNTLNQTYQOGTQVSMSMIDKIVDMMKVLSTIVDNKKFWQVTAATNTFTNLSQE 126
Db       66 AVVAYTDQTLSQSNQQSVMSMDRVTSVLIKTVMGVLSSG-SITQQTAAATDTFTNLTQK 124
Qy      127 SEAWIIFYKEDAHKSYYYNNILFALQDEETGGVNMATLPIAFDISYDIEKEKVLFTIKDT 186
Db       125 DSAWFWGKETSHQNYTNVMFAQNETIGRVMCVPGEIRVFTDKRTVLFLITKDY 184
Qy      187 ENYAVTVKAINVQALQSRSDSKVVD--AFKSPPHL 220
Db       185 ANYSYNIQTLRFAQPLIDSRLSINDLSEALRSSKYL 221
```

Search completed: June 26, 2005, 16:02:31
 Job time : 164 secs

CC insect management and provides a tool for management of insecticide
CC resistance. The present sequence represents a truncated delta-endotoxin
CC of B. thuringiensis isolate PS201T6 of about 25 kD. (Updated on 20-MAR-
CC 2003 to correct PF field.)

Sequence 222 AA;

```
Query Match 35.8%; Score 417; DB 2; Length 222;
Best Local Similarity 41.9%; Pred. No. 3.7e-32;
Matches 91; Conservative 42; Mismatches 72; Indels 12; Gaps 5;
Qy      15 DVVNYSEIXOVA-POVNQNLTLAKYFOGAI-----DGSTLRFDFEKAQIANDI-PQA 66
Db       6 DTTQLEITEENPVLYQLQIAQDAAFDALVPTEFGFAIRFSMPKGLEVAKTIQPKG 65
Qy      67 AVNTLNQTYQOGTQVSMSMIDKIVDMMKVLSTIVDNKKFWQVTAATNTFTNLSQE 126
Db       66 AVVAYTDQTLSQSNQQSVMSMDRVTSVLIKTVMGVLSSG-SITQQTAAATDTFTNLTQK 124
Qy      127 SEAWIIFYKEDAHKSYYYNNILFALQDEETGGVNMATLPIAFDISYDIEKEKVLFTIKDT 186
Db       125 DSAWFWGKETSHQNYTNVMFAQNETIGRVMCVPGEIRVFTDKRTVLFLITKDY 184
Qy      187 ENYAVTVKAINVQALQSRSDSKVVD--AFKSPPHL 220
Db       185 ANYSYNIQTLRFAQPLIDSRLSINDLSEALRSSKYL 221
```

Search completed: June 26, 2005, 16:02:31
 Job time : 164 secs

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OM protein - protein search, using sw model

Run on: June 26, 2005, 15:56:03 ; Search time 40 Seconds
(without alignments)
555.652 Million cell updates/sec

Title: US-10-767-605-2
Perfect score: 1165
Sequence: 1 MFFENRVTILTVPSDVVNTS.....DAFFKSPRHUPRKHKICNS 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9616763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79;*
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	54.7	259	2 S32432	toxin cytB - Bacil
2	456	39.1	249	2 A24044	28K crystal protein
3	456	39.1	249	2 B61595	28K parasporal cry
4	103	8.8	477	2 F71918	hypothetical prote
5	101	8.7	477	2 T30838	hypothetical prote
6	99.5	8.5	4540	2 A41874	cytoplasmic dynein
7	96.5	8.3	343	2 A31146	transcription repr
8	95.5	8.2	201	2 F61205	hypothetical prote
9	95.5	8.2	421	1 E91944	thymidine phosphor
10	95.5	8.2	1876	2 A83963	zinc metalloprotei
11	94.5	8.1	249	2 S69708	hypothetical prote
12	94.5	8.1	393	2 F83885	proteasome reg
13	92.5	7.9	4688	2 T32776	hypothetical prote
14	89.1	7.8	458	2 C81346	hypothetical prote
15	89.5	7.7	311	2 JQ2026	hypothetical prote
16	89.5	7.7	1363	2 D90550	outer layer protein
17	89	7.6	772	1 T41230	vsa-like (mycopla
18	89	7.6	1017	2 A61224	hypothetical TPR d
19	89	7.6	1389	1 T28247	bacilli
20	89	7.6	1805	1 D70174	hypothetical prote
21	88.5	7.6	717	2 F83909	ORF MSV086 probabl
22	88.5	7.6	735	2 B91092	methyl-accepting c
23	88.5	7.6	1447	2 A85938	hypothetical prote
24	88	7.6	458	2 A85938	probable invasion
25	88	7.6	646	2 A81587	bacteriophage prot
26	88	7.6	1636	2 S60403	probable membrane
27	87.5	7.5	390	2 S54026	ribosomal protein
28	87	7.5	488	2 T33750	hypothetical prote

RESULT 1
S32432
toxin cytB - Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S32432; S31476
R;Koni, P.A.; Ellar, D.J.
J. Mol. Biol. 229, 319-327, 1993
A;Title: Cloning and characterization of a novel Bacillus thuringiensis cytolytic delta
A;Reference number: S32432; MUID: 93156045; PMID: 8429550
A;Accession: S32432
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <XON>
A;Cross-references: UNIPROT:Q04470; EMBL:Z14147; PIDN:CAA78519.1; PID:94930·
C;Genetic:
A;Gene: cytB
C;Superfamily: 28K parasporal crystal protein

Query Match 54.7%; Score 637; DB 2; Length 259;
Best Local Similarity 56.0%; Pred. No. 1.2e-41;
Matches 126; Conservative 43; Mismatches 54; Indels 2; Gaps 2;

Qy 7 ITUTVPSDDVNNTFYVQPOYINQLHLANAFQGIDPLNNFNEKAQIANGIPI NSQE 66
Db 31 IUTVPSDDVNNTFYVQPOYINQLHLANAFQGIDPLNNFNEKAQIANGIPI NSQ 90
Qy 67 AVNTLNQTYQGTVQSYVMIDKIVMKVNTIVNKKFMDQVTAITTTFTNLSQE 126
Db 91 AVTKLNQSVIQQTQVBISWVQBLKLQIQBVGLVNSTSPNSVEATIKGIFTNLQDQI 150
Qy 127 SBAWIFIYKQEDAKHTSYNNILFAPQDGETGGMATLPIAFDISVDEKEKVLPVKTQD 186
Db 151 DEAWIFHSLSAHTNTSYNNILFSIQNDTGAVMAVLPLAPEVSVDYEVQKVLFTKIDS 210
Qy 187 ENYAVTVKAINVYQALLOSSRSOSKVDFAFK-SPRHLPPKRHKCLCSN 230
Db 211 ARYEVKMKALTIVQALHSS-NAPIVDIPVNVNNLYHSNHKCIQN 254

RESULT 2
A27520
28K crystal protein - Bacillus thuringiensis Plasmids
N;Alternate names: 28K cytolytic protein; delta-endotoxin
C;Species: Bacillus thuringiensis
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A27520; S06430
R;Ellar, D.J.; Ellar, D.J.
Nucleic Acids Res. 15, 3619, 1987
A;Title: Bacillus thuringiensis var. morrisoni strain PG14: nucleotide sequence of a gene
A;Reference number: A27520; MUID: 87203386; PMID: 3575104
A;Accession: A27520

A; Molecule type: DNA
A; Residues: 1-249 <PAA>
A; Cross-references: UNIPROT:P05069; GB:Y00135; NID:940260; PIDN:CRA68329_1; PMID:940261
A; Experimental sources: strain morrisoni PG14, 140Kb plasmid
R; Galjart, N.J.; Sivasubramanian, N.; Federici, B.A.
Cur. Microbiol. 16, 171-177, 1987
A; Title: Plasmid location, cloning, and sequence analysis of the gene encoding a 27.3-kDa protein
A; Reference number: S06430
A; Accession: S06430
A; Molecule type: DNA
A; Residues: 1-249 <PAA>
A; Cross-references: EMBL:M35968; NID:g143104; PIDN:AAA22553_1; PMID:g143105
C; Genetics:
A; Genome: plasmid
C; Superfamily: 28K parasporal crystal protein
C; Keywords: 28K parasporal crystal protein

Query Match 39.1%; Score 456; DB 2; Length 249;
Best Local Similarity 45.6%; Pred. No. 3.4e-29;
Matches 99; Conservative 44; Mismatches 64; Indels 10; Gaps 5;

Qy 5 RVITLTVPS-SDVNTVSEIYQV-AQYVNQALTLAKYFQGAI-----DGTSLRDFEKA 56
Db 25 RVITLTVEDPEINNLISNEIDNPNTYLQIMLANAQNALVPTSTDFDALRSMAKG 84
Qy 57 LQIANDI-POAVVNTLNQTYQOGTVQVSMDKIVDMDKVLNQVLSIVDNKCFWDQVTAI 115
Db 85 LEIANTITPMGAVVSVTDQNTQTNNQVSWINKVLELVKTVGLVAGLSGVT-DQJTAAV 143
Qy 116 TNTFTNLNSQEANLYFYKEDAHKTSYYNNILEAQDEETGYNMPLIAFDISVIDEK 175
Db 144 TNTFTNLNTQRNEAVWFWGKETANQNTVNLFAIQNAOTGVNYCVPGEIKVSAVK 203
Qy 176 EKVLFVTTIKDENTVATVTKAINVQVQALQSSRDVKVD 212
Db 204 EQVLTETIQDSASVNTNIQSUKFQAFLVQVSSQQYPAD 240

RESULT 4
B64595 hypothetical protein HP0605 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 03-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: B64595
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Lofthus, B.; Richardson, D.; Dodson, R.; Khaak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 338, 539-547, 1997
A;Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64220; PMID:7394467; PMID:252185
A;Accession: B64595
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-477 <TOM>
A;Cross-references: UNIPROT:O25326; GB:AB000574; GB:AB000511; NID:g21313721; PIDN:AAD07671

Query Match 8.8%; Score 103; DB 2; Length 477;
Best Local Similarity 20.5%; Pred. No. 1.3; Mismatches 54; Indels 38; Gaps 10;
Matches 47; Conservative 54; Mismatches 90; Indels 38; Gaps 10;

Qy 2 FPN--RVITLTVP---SSDVNVNSEIYQVAPQVNVQALTAKYFQGAI---DGSTLRF 51
Db 199 YPNNLARMIALQKKEQIKTIDKRVTKLIDKGTLTDDQLSKA-QGNLSEYD1LDMF 256
Qy 52 DFEKAQIANDIPOAVVNTLNQTYQOGTVQVSMDKIVDMDKVLNQVLSIVDNKCFWDQV 111
Db 257 ALBQRNLTEYLTNISVNLKTTIDAPNQLRERQD-LVSLREQISAIRYQKQI---- 311
Qy 112 TAAITNTFTNLNSQSEAWIIFYKEDAHKTSYYNNILEAQDEETGYNMPLIAFDISV 171
Db 312 ----NYPKCIDVFPDS-WLFWIQPKAVATGRFGN-FYPCQONTAQVATLNFDDIGL 362
Qy 172 DIEBKVLFTTIKDENYA-----VTVKAINVVA-LQSSRDS 208
Db 363 SLQKQSIMLGOLANEKLNAYKCLEQEKDELYRKSDIARAKIESSKA 411

A; Molecule type: DNA
A; Residues: 1-249 <PAA>
A; Cross-references: UNIPROT:P05069
A; Note: the authors translated the codon GAA for residue 204 as Gln
R; Gill, S.; Singh, G.J.P.; Hornung, J.M.
Infect. Immun. 55, 1300-1308, 1987
A; Title: Cell membrane interaction of *Bacillus thuringiensis* subsp. *israelensis* cyrolytic
A; Reference number: A60123; PMID:3570465
A; Accession: A60123
A; Molecule type: protein
A; Residues: 31-41 <GIL>
A; Note: this amino-terminal sequence was found in both 24K and 25K forms of the purified
R; Ward, E.S.; Biller, D.J.
J. Mol. Biol. 191, 1-18, 1986
A; Title: *Bacillus thuringiensis* var. *israelensis* delta-endotoxin. Nucleotide sequence and
A; Reference number: A24505; PMID:3025452
A; Accession: A24505
A; Molecule type: DNA
A; Residues: 1-249 <PAA>
R; Ward, E.S.; Biller, D.J.; Chilcott, C.N.
J. Mol. Biol. 202, 527-535, 1988
A; Title: Single amino acid changes in the *Bacillus thuringiensis* var. *israelensis* delta-

Qy	114 AITNTFTNLSQESEAWIY-----YKEDAHKTSYYNTILFAIQDEETGGWMATLPIA 166	Db	: 195 VA 196
Db	218 ALRSTFHSTNVEK---LFFGKINMLNQPFFHDTRVRSLSLIEKEQDVLKLVQSPHT 274		
Qy	167 EDISVDIBKEKVLFVTIKDTEN-----YAVTVAINTVQALQSSR 205		
Db	275 -GISIKIGKEN---DYEEMNCNLITASysVDOQKIGSIAIIGPTR 316		
RESULT 8			
A34146	hypothetical protein 603 - Autographa californica nuclear polyhedrosis virus	A;Species:	Mycoplasma genitalium
C;Date:	Autographa californica nuclear polyhedrosis virus, AcNPV	C;Sequence:	Mycoplasma genitalium
C;Accession:	A4146; S01094; G72850; F40781	C;Date:	23-Oct-1998 #sequence_revision 23-Oct-1998 #text_change 16-Aug-2004
R;Gearing, K.L.; Possee, R.D.	J. Gen. Virol. 71, 251-262, 1990	A;Title:	
A;Title:	Functional analysis of a 603 nucleotide open reading frame upstream of the poly	A;Status:	nucleic acid sequence not shown; translation not shown
A;Reference number:	A34146; MUID:90171909; PMID:2407804	A;Molecule type:	DNA
A;Accession:	A34146	A;Residues:	1-421 <TIGR>
A;Status:	Preliminary	A;Cross-references:	UNIPROT:P47297; GB:U39684; PIDN:93844650; PIDN:AACT1267.1;
A;Molecule type:	DNA	A;Experimental source:	strain G-37
A;Residues:	1-201 <GBA>	A;Genetic code:	SGC3
A;Cross-references:	UNIPROT:P24650; GB:D00700; EMBL:X06637; PIDN:9222181; PIDN:BA00606.1	C;Superfamily:	Thymidine phosphorylase/pyrimidine-nucleoside phosphorylase
A;Experimental source:	strain C6	C;Keywords:	glycosyltransferase; pentosyltransferase
R;Possee, R.D.; Howard, S.C.	Nucleic Acids Res. 15, 10233-10248, 1987	A;Query Match:	8.2% ; Score 95.5 ; DB 1 ; Length 421 ;
A;Title:	Analysis of the polyhedrin gene promoter of the Autographa californica nuclear	A;Best Local Similarity:	23.6% ; Pred. No. 4.5 ;
.A;Reference number:	S01094; MUID:88096564; PMID:3320964	A;Matches:	41; Mismatches: 75; Indels: 39; Gaps: 8 ;
A;Accession:	S01094	Qy	17 VNYSTIYQVAPQVNQALTLAKYFPGAIQDSTLRPDKFELQIANDIPQAVAVNTLNQTV 76
A;Molecule type:	DNA	Db	233 VKLSDMNQVLGKAVGNVIENE---AV--NFLQGQLDQVGQDFDLQMTQIVNLTLET 286
A;Cross-references:	EMBL:X06637; PIDN:CAA29845.1; PID:958429	Qy	77 QQGTYYQVSMDKTYDIDKQVLSIVTDNKKFWDQYTAITNTNTLNQSSEAWIIFYKE 136
R;Ayres, M.D.; Howard, S.C.; Ruzio, J.; Lopez-Ferber, M.; Possee, R.D.	Virology 202, 586-605, 1994	Db	287 QAKTKO-----KALBYQDVLT----SKCAWNRLPLSPI-----ESQGNVFLFTQKE 329
A;Title:	The complete DNA sequence of Autographa californica nuclear polyhedrosis virus	Qy	137 DAHKTSYYNNVILFAIODEBTGGWMTLPFAF-DISVDIEKEV-----LYFTIK 184
A;Reference number:	A72850; MUID:94303173; PMID:8030244	Db	330 GFFPKRY----KASTKAERKGILHPTDPIDLAKGICNLGARMKXTDQIDPMAGJFLMKC 385
A;Status:	Preliminary	Qy	185 DTENAVTVAIKNVVQALQSSRD 207
A;Molecule type:	DNA	Db	386 DNESTAVGDTVNLVSSSSPISNE 408
A;Residues:	1-95, 'M' 97-201 <AYR>	A;Query Match:	8.2% ; Score 95.5 ; DB 2 ; Length 201 ;
A;Cross-references:	GB:L22858; NID:9510708; PIDN:AAA66637.1; PID:g559076	A;Best Local Similarity:	22.5% ; Pred. No. 1.7 ;
R;Possee, R.D.; Sun, T.P.; Howard, S.C.; Ayres, M.D.; Hill-Perkins, M.; Gearing, K.L.	Virology 185, 229-241, 1991	A;Matches:	25; Mismatches: 59; Indels: 57; Gaps: 8 ;
A;Title:	Nucleotide sequence of the Autographa californica nuclear polyhedrosis 9.4 kbp	A;Reference number:	A40781; MUID:9204079; PMID:1926775
A;Accession:	F40781	A;Status:	Preliminary
A;Molecule type:	DNA	A;Residues:	1-95, 'M' 97-201 <PO2>
A;Cross-references:	GB:MF5679	A;Cross-references:	Streptococcus pneumoniae [Imported] - Streptococcus pneumoniae (strain R6)
C;Genetics:		C;Species:	Streptococcus pneumoniae
A;Gene:	Ac-ORF603	C;Date:	22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Qy	23 YQVAPQVNQALTL-----AKYFOGAIDGSTLRLPDKFELQIANDIPQ 65	C;Accession:	E97944
Db	29 YNILESYXVTPVLLKNGVIEEAAYAGNI---LYKTDDPKFDYINLIKATHSEELPS 85	R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Dehoff, B.S.; Ehrle, R.; Leblanc, D.T.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; McVay, P.; Sun, P.M.; Winkler, M.E.	
Qy	66 AAVNTLNQTVQGTVQVSMIDKUVDIMKNSIVDNKXF---MDQVTTAINTFTNLU 123	J. Bacteriol. 183, 5709-5717, 2001	
Db	86 NSTVNVYRKTSRSGTH-----PIKKDI---VYDNCFKFTLYDRYIYGDNVNNVFY 134	A;Authors:	Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
Qy	124 SQESEAWIIFTYKEDAHKTS-----YY---YNLFLAIQDDETBGGV 159	A;Title:	Genome of the Bacterium Streptococcus pneumoniae Strain R6.
Db	135 EBNKEKEKEYEEEDDKASILCENKILSQINCESPNDKFLSYDNYAFSIIIDNTNTVL 194	A;Reference number:	A97872; PMID:11544234
Qy	160 MA 161	A;Accession:	B97944
RESULT 9			
A;Status:	Preliminary	A;Molecule type:	DNA
A;Residues:	1-95, 'M' 97-201 <KUR>	A;Cross-references:	1-1876 <KUR>
A;Cross-references:	UNIPROT:08DQNS; GB:AB007317; PIDN:AAK99385.1; PIDN:AACT1267.1; GSPDB:G	C;Genetics:	
A;Experimental source:	strain C6H; P2:F40781 C;Acc (F40781) merged into P2:G72850 #date	A;Gene:	zmpB
A;Genetics:		A;Query Match:	8.2% ; Score 95.5 ; DB 2 ; Length 1876 ;
A;Gene:		A;Best Local Similarity:	20.4% ; Pred. No. 32 ;
A;Cross-references:		A;Matches:	41; Mismatches: 98; Indels: 41; Gaps: 9 ;

Query Match Score 94.5; DB 2; Length 393;
 Best Local Similarity 24.1%; Pred. No. 4.9;
 Mismatches 83; Indels 55; Gaps 16;
 Matches 57; Conservative 42; MisMatches 57;

Qy 30 VNQALTIAKYQGAIQGSTLRFDEKALQIANDIPQAVENTLNQVYQQGTVQVS---- 84
 Qy 73 INQ-LSVVKYLASLQDSK--DPDESLKYLDD--KAQFQELDSKKQRNNGSKDHGDGI 126

Db 85 VMIDKTV-----DIMK----NVLSIVDNEKFWMDQVTAATITFTNLNSQSESEAWI 131
 Db 127 LLDISBTARTYLLKNDIVKARDLDDLEKTLLKK--DSPIRINTSFYSTNSQ----Y 178

Qy 132 FVYKEDAHKTSYYNNILFAIQDEETGGVMAATL---PIAFDIDSVD-1KEKVV--- 178

Db 179 FKFKNDEN--SFYTTSLSLYLSTLEP-STSTIAERQOLAYDLISIALLGDIYNFGFLHH 228

Qy 179 -LFTIKDTENAVTVKAINVVAQLOSSR-DSKV-YDAFKSP-- -RHLPRKGHKIC 228

Db 236 HPIMETVNDSNYDWFQLLNALTGVDFDKPDSLKVQISKIPILAQHESPURQKIC 292

RESULT 11

A83963 hypothetical protein BH2505 [imported] - *Bacillus halodurans* (strain C-125)
 C;Species: *Bacillus halodurans*
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: A83963
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A;Reference number: A83650; MUDB:20512582; PMID:11058132
 A;Accession: A83963
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-249 <SRO>
 A;Cross-references: UNIPROT:Q9K9Y9; GB:AP001515; GB:BA000004; PIDN:BA062
 A;Experimental source: strain C-125
 C;Genetics: BH2505
 C;Superfamily: conserved hypothetical protein yloO; conserved hypothetical protein yloO
 Query Match Score 94.5; DB 2; Length 249;
 Best Local Similarity 21.0%; Pred. No. 2.7;
 Matches 37; Conservative 38; Mismatches 64; Indels 37; Gaps 7;

Qy 62 DIPQAAVNTLNQTVQGTVQVSMI-----DKIVDIMKRNVLIVDNKFWMDQVTAI 115
 Db 8 DVGKVPRHNBONGTIMEKGQLVYVADGMGSHQAGDVASKWATELL-KREWERS--- 62

Qy 116 TNTPTNQSEBAAWIFYKEDAHKTSYYNNILFAIQDEETGGVMAATLPIAFDISVIBK 175
 Db 63 ---LSPSQSEBEGMLRNQVHLHNESLHY---AQRHEECOGMTL---VAAIVDK 109

Qy 176 EKVLFVTIKDTENAVTVKAINVVAQLOSSRDSKVUDAF-----KSPRLPLRK 223
 Db 110 BRTVIAHIGDSRAYLINEHGFS----QKTRDHSLYNVELRTGQISDEAHHPRK 160

RESULT 12

S69708 26S proteasome regulatory particle chain RP9N - yeast (*Saccharomyces cerevisiae*)
 N/Alternate names: protein YDR427w
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 A;Accession: S69708
 R;Dietrich, F.S.
 Submitted to the EMBL Data Library, August 1995
 A;Description: The sequence of *S. cerevisiae* lambda 3641 and cosmids 9461, 9831, and 941
 A;Accession number: S69555
 A;Accession: S69708
 A;Molecule type: DNA
 A;Residues: 1-393 <DIE>
 A;Cross-references: UNIPROT:Q04062; EMBL:U33007; PID:927685; GSPDB:GN00004
 C;Genetics: SCP:RP9N; RP9N; MIPS:YDR427w
 A;Gene: SCP:RP9N; RP9N; MIPS:YDR427w; SGD:S0002835
 A;Cross-references: MIPS:YDR427w; SGD:S0002835
 A;Map position: 4R
 A;Title: The complete genome sequence of *Escherichia coli* K-12.

RESULT 13

F82885 hypothetical protein UU482 [imported] - *Ureaplasma urealyticum*
 C;Species: *Ureaplasma urealyticum*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: F82885
 R;Glass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to Genbank, February 2000
 A;Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a mi:
 A;Reference number: A82870
 A;Accession: F82885
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-468 <GLA>
 A;Cross-references: GB:AB002145; GB:AF222894; NID:96899476; PIDN:AAF30894.1; GSPDB:GN001
 A;Experimental source: serovar 3; biovar 1
 C;Genetics:

Query Match Score 92.5; DB 2; Length 4688;
 Best Local Similarity 22.3%; Pred. No. 1.9e+02;
 Matches 44; Conservative 32; Mismatches 72; Indels 49; Gaps 8;
 A;Gen: UU482
 A;Genetic code: SGCG3

Qy 51 FDFBKALQIANDI-PQAAVNTLNQTVQGTVQVSMIDKIV--DIMKVNLSIVDNNKK 106
 Db 1509 YDEQNKISLSNNINNPYSYKPTQINQKDSYNDVNLQVDKQLLNLKQLNNDNKT 1568

Qy 107 FW-DQV---TAATNTFTNLNSQSEBAAWIFYKEDAHKTSYYNNILFAIQDEETGGVMA 161
 Db 1569 VWTDPILENNNAKISPKFLSNL-----IHNTAYELEG1YYFPDQNSYNDMT 1613

Qy 162 TLPFAFDISV--DIEKEKVLFVTIKDTENAVTVKAINVVAQLOSSRDSKVUDAF-----VHQ 200
 Db 1614 NNQISPNSKH1HKPKC1FEPSSLTNTDNNNAKITS1SAHNAQVHPKLTNDBALENDQIVE 1673

Qy 201 AL---QSSRDSKVYDA 213
 Db 1674 AVFAPTNLNQKQVYEA 1690

RESULT 14

B65068 hypothetical protein b2852 - *Escherichia coli* (strain K-12)
 C;Species: *Escherichia coli*
 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
 C;Accession: B65068
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
 A;Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of *Escherichia coli* K-12.

A; Reference number: A64720 ; MUID:97426617 ; PMID:9278503
A; Accession: E6068
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-158 <BLAT>
A; Cross-references: UNIPROT:P76639 ; GB:AE000369 ; GB:U00096 ; PID:92367168 ; PIDN: AAC75891.
A; Experimental source: strain K-12, substrain MG1655

Query Match 7.8%; Score 91; DB 2; Length 458;
Best Local Similarity 20.3%; Pred. No. 12; Indels 44; Gaps 8;
Matches 45; Conservative 37; Mismatches 96; Indels 44; Gaps 8;

Qy 21 IYQVAPQVNQALTLAKYFQGAIDSTLRFD----FEKALQIANDIPQAQAVNTLNQT 75
Db 265 ELYDFPESITRADMFLDQLQNSDITQTLERPECYCLAECTMSLA----- 309

Qy 76 VQQGTVQYSWMDKIVDLMKRNVLSI-VIDDNKFKWDQVTAATNTFTNLNSQESEAWIFFYY 134
Db 310 -LHGKSSLEAAQKALDLDVSDITVDGK-----ILAIMGLLTGSGAQVSHLFE 362

Qy 135 KEDAHRTS---YKYNILPAIQDEEFQGVMMATLPIAFDISDIEKEKVLVFTVTKTENYA 190
Db 363 QAKIHSTDIASLYYPSALVHFINEK---IEBARICIDKS1QLEPRRRAVVIKECVDDMY 418

Qy 191 VTVKAINVQALQSSRDK---VVDAKSPSPHLPKRKHIC 228
Db 419 VNPPLKNIKLYKEPESSEHVVIIKLUKQJLR--IC 456

RESULT 15
T32776 hypothetical protein D1069.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_change 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32776
R;Murray, J.; Langston, Y.; Clarke, K.; Morris, M.
Submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid D1069.
A;Reference number: Z21223
A;Accession: T32776
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-311 <MGR>
A;Cross-references: UNIPROT:O44789 ; EMBL:AF040641 ; PIDN: AAB94946.1 ; GSPDB: GN000020 ; CBSP :
A;Experimental source: strain Bristol N2; Clone D1069
C;Genetics:
A;Gene: CE8P:D1069.1
A;Map position: 2
A;Introns: 264/3
C;Superfamily: Caenorhabditis elegans hypothetical protein D1069.1

Query Match 7.7%; Score 89.5; DB 2; Length 311;
Best Local Similarity 21.7%; Pred. No. 9.1; Indels 41; Gaps 6;
Matches 36; Conservative 29; Mismatches 60; Indels 41; Gaps 6;

Qy 22 IYQVAPQVNQALTLAKYFQGAIDSTLRFDPEKALQIANDIPQAQAVNTLNQT/QQGTV 81
Db 138 VIGVRHQYKTSEFSQNKFPSKKIDS--FFEFLISRSQSKIFKILIS-KQKLRKFPF 192

Qy 82 QVSVMIDK-----IVDIMKVNLSI-----VIDNKFKWDQV-----AAI 115
Db 193 QVVRPSQSAMLRGGYANVVNLSTQKLQIAQIRSISFSIRTMWDEVNSWFTKSPKAVI 252

Qy 116 TNTFTNLNSQESEAW-----IIFYKEDAHKTSYYNNILFAI 151
Db 253 INFFSDQSAMPNQFWGQYTGKIKKCLUFFSBDLDRNPFANILVLI 298